

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 00:16:37 ; Search time 10533 Seconds
(without alignments)
11252.122 Million cell updates/sec

Title: US-10-782-570-3
Perfect score: 2085
Sequence: 1 atgtgtcaagggaatacaca.....caaatatgatattgattaa 2085

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vl.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, ... and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2085	100.0	2085	6	CQ868309	CQ868309 Sequence
2	2085	100.0	2235	6	CQ868307	CQ868307 Sequence
3	1794.4	86.1	2208	6	CQ868305	CQ868305 Sequence
4	334.6	16.0	3543	1	BTTOXD1	Y00423 Bacillus th
5	334.6	16.0	4253	1	BACISRH4	D00248 Bacillus th
6	334.6	16.0	4451	6	I08083	I08083 Sequence 1
7	334.6	16.0	4451	6	I09103	I09103 Sequence 1
8	334.6	16.0	4934	6	E01676	E01676 DNA sequenc
9	334.6	16.0	127923	1	BTBPTOXIS	AL731825 Bacillus
10	221.8	10.6	6009	1	BTH251977	AJ751977 Bacillus
11	202.8	9.7	434	1	DQ078744	DQ078744 Bacillus
12	190.8	9.2	4959	1	AF285775	AF285775 Bacillus
13	180.4	8.7	3752	1	AB125059	AB125059 Bacillus
14	170	8.2	3642	1	AB193814	AB193814 Bacillus
15	161.2	7.7	4896	1	AF132928	AF132928 Bacillus
16	159.6	7.7	127923	1	BTBPTOXIS	AL731825 Bacillus
17	158	7.6	3753	1	BACMSQB	M12662 B.thuringie
18	146.6	7.0	3756	6	E00614	E00614 DNA encodin

19	144	6.9	3644	1	BTH251978	AJ251978 Bacillus
20	117	5.6	15548	6	AX347057	AX347057 Sequence
21	112.4	5.4	1993	1	I03578	I03578 Sequence 1
22	105.8	5.1	133877	14	AC120883	AC120883 Homo sapi
23	100.6	4.8	3535	6	I06096	I06096 Sequence 2
24	100.6	4.8	3684	1	BTTOXD2	X07082 Bacillus th
25	100.6	4.8	3684	1	BTTOXD2	X07423 Bacillus th
26	100.6	4.8	3684	6	I08884	I08884 Sequence 2
27	99.4	4.8	1738	6	I03580	I03580 Sequence 3
28	99.4	4.8	17870	8	AC104073	AC104073 Homo sapi
29	99.2	4.8	349980	6	AX344555	AX344555 Sequence
30	99	4.7	4186	1	BACISRH3	D00247 Bacillus th
31	99	4.7	4186	6	E01905	E01905 genomic DNA
32	98.2	4.7	72243	8	AL731858	AL731858 Human DNA
33	97.8	4.7	3536	6	E01029	E01029 DNA sequenc
34	97.8	4.7	4056	1	BACCRD2	M20242 B.thuringie
35	96.8	4.6	254050	2	PF329358	AL293158 Plasmodiu
36	96	4.6	104992	14	AC005504	AC005504 Plasmodiu
37	96	4.6	169546	14	AC004157	AC004157 Plasmodiu
38	96	4.6	176898	8	AC117569	AC117569 Homo sapi
39	96	4.6	250421	2	AE014849	AE014849 Plasmodiu
40	95	4.6	3668	1	D88381	D88381 Bacillus th
41	94.4	4.5	110000	14	PFMAL0P1_05	Continuation (6 of
42	93.6	4.5	8056	6	AX599046	AX599046 Sequence
43	93.6	4.5	348174	2	CR382399	CR382399 Plasmodiu
44	92.6	4.4	3507	1	BTU04365	U04365 Bacillus th
45	92.6	4.4	3507	6	I25972	I25972 Sequence 3

ALIGNMENTS

RESULT 1	CQ868309	Sequence 10 from Patent WO2004074462.	2085 bp	DNA	linear	PAT 13-SEP-2004
LOCUS	CQ868309					
DEFINITION	CQ868309					
ACCESSION	CQ868309.1	GI:51998355				
VERSION						
KEYWORDS						
SOURCE	Bacillus thuringiensis					
ORGANISM	Bacillus thuringiensis					
REFERENCE	1	Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B.				
AUTHORS		Delta-endotoxin genes and methods for their use				
TITLE		Patent: WO 2004074462-A 10 02-SEP-2004;				
JOURNAL		Athenix Corporation (US)				
FEATURES		Location/Qualifiers				
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		1..2085				
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		/db_xref="GI:51998355"				
		/translation="MCQNTQYGDNFETASADTIAAVSAGTIVSGTLLAGIGGLTST				
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		LEGPRQLQSYNTALDDWRKLRLQARQLPSSALQQAALTKIRFNVHDFIREIP				
		GFQETVTKLLLPYAAQANFHLNLQGAELADENADHPISOENAGVSDDYKYL				
		LKENPKYSNCANTYREGNKLNRNENRSIFENDRYRNTITVLTDTIAQSPYDIK				
		RYKDSIGRIGIKTELREIYTTINFDRLTLEIQNLAIMEYLNTRSGURLFSLD				
		ELIYTKNETYGNRLVGIANRSTYATGTETIYGERTPPTTKLIPFSYKVSIV				
		TDRVTPSPPNFYFTINOELYNNSPNKLTYSAGNLSNKKTKTDFQPVKDC				
		XIIITNPLPSYNSYSHLSQFSFYTKYKGLALNLTGALGWTHTSVNRNNAISD				
		KLIITMFAIKGNSLDTNSKTEGRTGCHGNLYVLOSQRLEITCTNSTQSYIYLR				
		YATNGAGNTLPNISLTIPVIGIPQPLNNFTSGTNVNNLQYGFQGFQFPSTVLP				
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		TLNTEATNYDID"				

ORIGIN

Query Match 100.0%; Score 2085; DB 6; Length 2085;									
Best Local Similarity 100.0%; Pred. No. 1.5e-271;									
Matches 2085; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	ATGTGTCAGGGAAATACACAATATGGTGATAATTTTCGAGACATTTGCTAGTGCCTGATACA	60						
Db	1	ATGTGTCAGGGAAATACACAATATGGTGATAATTTTCGAGACATTTGCTAGTGCCTGATACA	60						
Qy	61	ATTGCTGCAGTTAGTCAGGTACTATTGTATCCGGTACTCTGTTCGCGGTATAGTGGG	120						
Db	61	ATTGCTGCAGTTAGTCAGGTACTATTGTATCCGGTACTCTGTTCGCGGTATAGTGGG	120						
Qy	121	CTCACTTCTATATCCGACCGATAGGAATATAGTGGCTATATATATATCTTTTGTGACC	180						
Db	121	CTCACTTCTATATCCGACCGATAGGAATATAGTGGCTATATATATATCTTTTGTGACC	180						
Qy	181	CTAATCACTGCTCTTTTGGCCGGGAGAACAGACAAAAACAGTATGGACACAATTTATT	240						
Db	181	CTAATCACTGCTCTTTTGGCCGGGAGAACAGACAAAAACAGTATGGACACAATTTATT	240						
Qy	241	AAAAATGGGAGAAATTTTGTGTATACACCGTTAACAGAAAGCATAAAAACAGCTAAAGTTA	300						
Db	241	AAAAATGGGAGAAATTTTGTGTATACACCGTTAACAGAAAGCATAAAAACAGCTAAAGTTA	300						
Qy	301	CAAACTTTAGAGGATTTAGACAAATATTACAAAGCTATTAATACAGCATTTAGATGTTGG	360						
Db	301	CAAACTTTAGAGGATTTAGACAAATATTACAAAGCTATTAATACAGCATTTAGATGTTGG	360						
Qy	361	AGAAAATTAAGAGATACAAAGCTCTGGATTACCAACCATCATCAGCATTTACAAACAGCT	420						
Db	361	AGAAAATTAAGAGATACAAAGCTCTGGATTACCAACCATCATCAGCATTTACAAACAGCT	420						
Qy	421	GCCTTGACTCTTAAATACGATTTGAGAAATGTTTCAAAATGATTTTATTCGAGAAATACCT	480						
Db	421	GCCTTGACTCTTAAATACGATTTGAGAAATGTTTCAAAATGATTTTATTCGAGAAATACCT	480						
Qy	481	GGTTTCCAACTTGAACCTTATAAAACGCTATTACTACCTATTTATGGCGAAGCTGCTAAT	540						
Db	481	GGTTTCCAACTTGAACCTTATAAAACGCTATTACTACCTATTTATGGCGAAGCTGCTAAT	540						
Qy	541	TTTTCATTTAAATTTATTACAAACAGGTGCTGAATGGCTGATGAATGGAAATGCAGATATA	600						
Db	541	TTTTCATTTAAATTTATTACAAACAGGTGCTGAATGGCTGATGAATGGAAATGCAGATATA	600						
Qy	601	CATCCTTCAAAATGGAACCTAATGCTGGAAACATCAGATGACTATTATATAAATTTTAAAA	660						
Db	601	CATCCTTCAAAATGGAACCTAATGCTGGAAACATCAGATGACTATTATATAAATTTTAAAA	660						
Qy	661	GAAAAATACCTAAATATAGTAATCTATTGTGCAAAATACCTATAGAGAGGACTTAAATAAA	720						
Db	661	GAAAAATACCTAAATATAGTAATCTATTGTGCAAAATACCTATAGAGAGGACTTAAATAAA	720						
Qy	721	CTTTCGAAACGAACTAATATAGATGGAGTATATTTAAATGATTTATCGAAGATATATGACT	780						
Db	721	CTTTCGAAACGAACTAATATAGATGGAGTATATTTAAATGATTTATCGAAGATATATGACT	780						
Qy	781	ATTACTGTATTAGATACTATCGCTCAATTTTCTTTTATAGATATAAGAGATACAAAGAT	840						
Db	781	ATTACTGTATTAGATACTATCGCTCAATTTTCTTTTATAGATATAAGAGATACAAAGAT	840						
Qy	841	TCAATAGGAAGATAGTGGCATTAAACCTGAACCTTACAGAGAAATTTTATACAACTGAA	900						
Db	841	TCAATAGGAAGATAGTGGCATTAAACCTGAACCTTACAGAGAAATTTTATACAACTGAA	900						
Qy	901	ATAAATTTTACCGCTCTTACTTACCTTGAATTTCAACCCCAATCTCGCTATAATGGGAATAT	960						
Db	901	ATAAATTTTACCGCTCTTACTTACCTTGAATTTCAACCCCAATCTCGCTATAATGGGAATAT	960						
Qy	961	AATTTTAAACGCTTCAGGGCTTAGATTTATTTTCAATTTTATTTAGATGAACTTATTTTATACA	1020						
Db	961	AATTTTAAACGCTTCAGGGCTTAGATTTATTTTCAATTTTATTTAGATGAACTTATTTTATACA	1020						

Qy	1021	AAAAATGAAACGTCGCGGAATCGTTAGTTGGTATTTGCGAAATCGTAATAGATCTACTTAT	1080						
Db	1021	AAAAATGAAACGTCGCGGAATCGTTAGTTGGTATTTGCGAAATCGTAATAGATCTACTTAT	1080						
Qy	1081	GCTACGACAGGAACTGAAATTTATATATGGAGAAAAGAACAGGTCACCCACACAAAAAAT	1140						
Db	1081	GCTACGACAGGAACTGAAATTTATATATGGAGAAAAGAACAGGTCACCCACACAAAAAAT	1140						
Qy	1141	TTAATACCAATTTTGAATCCTATATAAGTTTCAATTTGTAACCTGATAGACAGTAATCTACT	1200						
Db	1141	TTAATACCAATTTTGAATCCTATATAAGTTTCAATTTGTAACCTGATAGACAGTAATCTACT	1200						
Qy	1201	TCCCTCTTTTCCCTAAACATATACCTTAAATTAATCAAAATTTGAACTTTTAAATAATTTCA	1260						
Db	1201	TCCCTCTTTTCCCTAAACATATACCTTAAATTAATCAAAATTTGAACTTTTAAATAATTTCA	1260						
Qy	1261	CCTAGTAATAAATTTAAACATATTTACGCTGGGGGAAATTTTCTAATGATAAAAACAAT	1320						
Db	1261	CCTAGTAATAAATTTAAACATATTTACGCTGGGGGAAATTTTCTAATGATAAAAACAAT	1320						
Qy	1321	GATTTTCAATTTTCCCTGTAATAAAAGACTGTAAACCAATTTATTAAATTTGTTTACCA	1380						
Db	1321	GATTTTCAATTTTCCCTGTAATAAAAGACTGTAAACCAATTTATTAAATTTGTTTACCA	1380						
Qy	1381	AGCTATAATAGTTATAGTATATTTTATCCCAAGTTTCTTTTAAATTTTCTTAAATAA	1440						
Db	1381	AGCTATAATAGTTATAGTATATTTTATCCCAAGTTTCTTTTAAATTTTCTTAAATAA	1440						
Qy	1441	ATTGGAATAGCCCTAAATATATATATACAGGTGCATTTAGGATGGACACACAGTAGTGT	1500						
Db	1441	ATTGGAATAGCCCTAAATATATATATACAGGTGCATTTAGGATGGACACACAGTAGTGT	1500						
Qy	1501	ATAGAAATAATGCAATATCAGATAAAATTAATCAATGATCCCAAGCAATCAAGGTAAAC	1560						
Db	1501	ATAGAAATAATGCAATATCAGATAAAATTAATCAATGATCCCAAGCAATCAAGGTAAAC	1560						
Qy	1561	AGTCTTGATACAAACTCTAAAGGTAATTTGAAGGACCTGGTTCATACAGGAGGAAACCTTGGTT	1620						
Db	1561	AGTCTTGATACAAACTCTTAAGGTAATTTGAAGGACCTGGTTCATACAGGAGGAAACCTTGGTT	1620						
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Db	1621	TATTTACAAAGTCAAGGGGTTTAGAGATTAATGTAGAACTCCTTAATTTCTACAAATCT	1680						
Qy	1681	TATTTACATTTAGACTTCGATACCAATGCTGCTGGAATACTCTTCTTAATATATCT	1740						
Db	1681	TATTTACATTTAGACTTCGATACCAATGCTGCTGGAATACTCTTCTTAATATATCT	1740						
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Db	1741	CTTACAATACCAAGGATTAAGGAATACCACCTCAACGACTCAACAACTTTTCTGGT	1800						
Qy	1801	ACAAATTAATAATTTTACAATACGAGATTTTGGTATTTCCAAATTTCCAGTACAGTA	1860						
Db	1801	ACAAATTAATAATTTTACAATACGAGATTTTGGTATTTCCAAATTTCCAGTACAGTA	1860						
Qy	1861	ACATTTACCTTTTAAATCGGAACATACCATTTATTTAATCGTGACAGATGTATCAAAATTTCA	1920						
Db	1861	ACATTTACCTTTTAAATCGGAACATACCATTTATTTAATCGTGACAGATGTATCAAAATTTCA	1920						
Qy	1921	ATTTTAAATCATTTGATAAAATTTGAATTTTATACAAATTTCTTCTGTGACGCAAAATAGTA	1980						
Db	1921	ATTTTAAATCATTTGATAAAATTTGAATTTTATACCAATTTCTTCTGTGACGCAAAATAGTA	1980						
Qy	1981	GAAAAACAAAAATTTAGAACTATCCAAACAAAAATAAATACATTTTTCACAAATCATACA	2040						
Db	1981	GAAAAACAAAAATTTAGAACTATCCAAACAAAAATAAATACATTTTTCACAAATCATACA	2040						
Qy	2041	AAAAATACCTTTTAAATATAGAGCCCAAACTATGATTTGATTTAA 2085							
Db	2041	AAAAATACCTTTTAAATATAGAGCCCAAACTATGATTTGATTTAA 2085							

994	TC	AATAGGAGGAATAAGAGTAAAGGCACTAAGATGAACTCAAGAGAGAAATTTATACA	1053
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955	GA	ATAATAATTTTAAACGCTTCAGGCGCTTAGATATATTTTCATTTTGTAGATGAATTAATTT	1014
1114	GA	ATAATAATTTTAAACGCTGCAAGTGTTTTAAATATATTTTCATTTTGTAGAACAAATTAATTTT	1173
1015	TAT	CAAAAAAATCGAAGTACGGGAATCGTTTATGTTGTTATTCGCGAATCGTAAATGATCT	1074
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1075	ACT	TATGCTACGACGAGAACTGAAAATATATATATGAGAGAAAGAACAGGTCCACCCACAACA	1134
1234	ACT	TATAGCAATATCTATACTGAACTTTATATATGAGAGAAAGAACAGGTTCACCCACAACA	1293
1135	AAA	ACTTTTAATACATTTTGAATCCTATAAAGTTTCAAATTTGTTAACTGATAGACAAGTAACT	1194
1294	AAA	CAATAAGACCATTTTGAATCTTATAAAGTTTCAAATTTGTTAACTGATAGACAATCACCT	1353
1195	CGT	ACTTCCCTTTTCCCTAACATATACTTTTCAATTAATCAAAATTCGAATCTTTATTTAAAT	1254
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1411	GG	CTCATCTAACACACACTCAAAATTTCAAGCAGGAGGGTCTTTATCTAATTAACAAC	1470
1315	ACA	ACTGATTTTCAAATTTCTGTAAAAAAGACTGTAAACCAATTAATTAATCCAAATTTGT	1374
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1591	TAT	GTGATTTGATTTACAGCTTACAATATTTAGATACAGGTGCTATTAGGATGGACACACAGT	1650
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1555	GG	TAACTCTTGTATACAAACTCTAAGGTAAATTTGAAGGACCTGGTCTATACAGGAGGAAC	1614
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1795	TCT	GGTACAAATTAATAATTTTACAATACGAGATTTTGGGTATTTTCCAAATTTTCCAAGT	1854
1951	TCT	GGTACAAATTAATAATTTTACAATACGAGATTTTGGGTATTTTCCAAATTTTCCAAGT	2010
1855	AC	AGTAAACATTTACCTTTTAAATTCGAAACATACATTTATTTAATTCGTGCAGATGTATCA	1914
2011	AC	AGTAAACATTTACCTTTTAAATTCGAAACATACATTTATTTAATTCGTGCAGATGTATCA	2070
1915	AA	TTCAAATTTTAACTTATGATAAAATTTGAAATTTTATACCAATTAATCTCTCTGTACGCCAA	1974
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[illegible]

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/citation=[2]

ORIGIN

Query Match 16.0%; Score 334.6; DB 1; Length 3543;
Best Local Similarity 53.9%; Pred. No. 4.9e-36;
Matches 858; Conservative 0; Mismatches 695; Indels 38; Gaps 7;

QY 499 TATAAAGCGTATTACTACCTATTTATGCGCAAGCTGCTAAATTTTCATTTTAAATTTATTA 558
DB 604 TATAACATACTAGTATTATCTAGTTATGCAACAGCAGCAAACTTACATCTGACTGTATTA 663
QY 559 CAACAAGGCTGCTGAATGGCTGATGAATGGAATGCGAGATATACATCCTTCACAAATGAA 618
DB 664 AATCAAGCCGTCAAATTTGAAGCGTATTTAAAAAACAATCGACAAATTCGATTTATTAGAG 723
QY 619 CCTAATGCTGGAACATCAGATGACTATTATAAACTTTTAAAGAAATAATACCTAAATAT 678
DB 724 CCTTTGCC---AAAGCAATTGATTATTTATCCAGTATGCTAAGCTATAGAGATTAC 780
QY 679 AGTAACCTATTGTGCAATACCTATAGAGAGAGACTAAATAAACTTCGAACGAACTAAAT 738
DB 781 ACTAATTTATGCTGAACAATTTATAAAAGAGATTAAATTTAAATTAATAAAGCGCTGAT 840
QY 739 ATGAGATGGATATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT 798
DB 841 AGTAATCTTGATGGAATATAAATCGGAACACATACATACTGATCGAACAATAAATGACT 900
QY 799 ATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAATAAGGT 858
DB 901 ACTGCTGATTAGATGTTGTGCACTTCTTCCTAATTTATGATGATGATTAATCCAAAT 960
QY 859 GGCATTTAAACTGAACCTTACAGAGAAATTTATCAACTGAAATTAATTTTGACCGTCT 918
DB 961 GGTGTCCAATCTGAACCTTACTCGAGAAATTTAT-----CAGGTACTTAACCTTCGAAGA 1013
QY 919 ACTTACCTTGAATTTCAACCAATCTCGCTATTAATGGAATATTAATTTAACACGCTTCAGG 978
DB 1014 AAGCCCTATAAATATTATGACTTTCAATATCAAGAGGATTCATCTACAGTACAGCCGA 1073
QY 979 CTTAGATATTCTTCAATTTTATGATGAATTTATTTATCAAAAAATGAAAGTACGGG 1038
DB 1074 TTTATTTACTGGCTGATCTTTGATTTTATGAAAGGCGCAAACTACTCTTAATAA 1133
QY 1039 AATCGTTTATGTTGATTCGGAATCGTAATAGATCTACTTT-ATGCTACGACAGGAATGA 1097
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QY 1098 AATTATATGGAAGAAGACAGGTCCACCACACAAAACTTTTAATACCATTTTGAATC 1157
DB 1194 TAGTGTGTTTGGAAATCACAATGTAACTGATAAATTAATAATCTCTTGGTTGGCAACAA 1253
QY 1158 CTATAAGTTTCAATTTGTAAGTATGATAGACAAAGTAAGTCTTACTTCCCTTTTCTTCAACAT 1217
DB 1254 TATTTATATTTTTTATTAAGTCTATAGCTTAGATATAATAATCTAAATGATTATAA 1313
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DB 1314 TAATATTAGTAAATGGATTTTTTTTATACTAATAGTACTAGACTTTTGGAGAAGAAGT 1373
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QY 1338 AAAAAAGACTGTAAACCAATTAATTAATCCAAATTTGTTTACCAGCTATAATAGTTATAG 1397
DB 1434 TCTTAAACGAGAGATCAAGAAACCCCTACCTTTTCCACATATGATTAATAGTAG 1493
QY 1398 TCATATTTTATCCAGGTTTCTTTTATTAATTAATTCCTATAAATTTGGATAGCGCTAA 1457
DB 1494 TCATATTTTATCATTTTATTAAGAGTCTTAGTATCCC-----TGCAACATA 1538
QY 1458 TATATTTATACAGGTGCATTAGGATGGACACACACTAGTGTGTTAATAGAAATAATCCAT 1517

DB 1539 TAAAACTCAAGTGATACGTTTGGACACACTCTAGTGTGATCCCTAAAAATACAT 1598
QY 1518 ATCAGATAAAATAATTTACAATGATCCAGCAATCAAAGGTAACAGTCTTTGATACAAACTC 1577
DB 1599 TTATACACATTTAACTACCAAAATTCAGCTGTAAAAGCAATTCACCTTTGGGACTGCTTC 1658
QY 1578 TAAAGTAATTGAAGACCTGTCATACAGGAGAAACTTGGTTTATTTTACAAAGTCAAG 1637
DB 1659 TAAAGTTGTTCAAGACCTGGTCATACAGAGGGGATTTAAATTTGATTTCAAGATCA--- 1715
QY 1638 GCGTTTAGAGATTACATGTAGAACTCTAATTTCTACACAATCTTATTACATTAGACTTCG 1697
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BACISR4
LOCUS
DEFINITION
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insecticidal protein (ISR4), complete cds.
ACCESSION
D00248
VERSION
D00248.1
KEYWORDS
130 kDa insecticidal protein (ISR4).
SOURCE
Bacillus thuringiensis serovar israelensis
ORGANISM
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE
1 (bases 1 to 4253)
AUTHORS
Sen.K., Honda.G., Koyama.N., Nishida.M., Neki.A., Sakai.H., Himeno.M. and Komano.T.
TITLE
Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes of Bacillus thuringiensis var. israelensis
JOURNAL
Agric. Biol. Chem. 52, 873-878 (1988)
COMMENT
The genes of ISR3 and ISR4 that were 130 kDa insecticidal proteins of Bti were sequenced and compared with other insecticidal protein genes. ISR3 and ISR4 were identical in a region of the C-terminal 467 amino acids.
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ORIGIN

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Best Local Similarity 53.9%; Pred. No. 4,5e-36;
Matches 858; Conservative 0; Mismatches 365; Indels 38; Gaps 7;

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DEFINITION
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AUTHORS
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1964
1039
2024
1098
2084
1158
2144
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Sequence 1 from Patent EP 0296870.
108083
108083.1
GI:589204
Unknown.
Unclassified.
1 (bases 1 to 4451)
Ellar,D.J. and Ward,E.S.
New toxin-encoding DNA fragments from *Bacillus thuringiensis*
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109103
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VERSION
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REFERENCE
109103
Sequence 1 from Patent WO 8810305.
109103
109103.1
GI:588188
Unknown.
Unclassified.
1 (bases 1 to 4451)

AUTHORS Ellar,D.J. and Ward,E.S.
JOURNAL Patent: WO 8810305-A 1 29-DEC-1988;
FEATURES Location/Qualifiers
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Query Match 16.0%; Score 334.6; DB 6; Length 4451;
Best Local Similarity 53.9%; Pred. No. 4.4e-36;
Matches 858; Conservative 0; Mismatches 695; Indels 38; Gaps 7;
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RESULT 8

E01676 LOCUS 4934 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA sequence encoding Bacillus thuringiensis insectivorous protein.
ACCESSION E01676
VERSION E01676.1 GI:2169929
KEYWORDS JP 1988230090-A/1.
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 4934)
AUTHORS Komano, T. and Himeno, M.
TITLE INSECTICIDAL PROTEIN OF STRAIN BACILLUS THURINGIENSIS VAR
JOURNAL Patent: JP 1988230090-A 1 26-SEP-1988;
COMMENT OS Bacillus thuringiensis
PN JP 1988230090-A/1
PD 26-SEP-1988
PF 19-MAR-1987 JP 1987066844
PI KOMANO TORU, HIMENO MICHIO
PC C12N1/00, A01N63/00, C12N1/20, C12P21/02, C12N1/02, (C12N1/20,
PC C12R1:19);
CC strandedness: Double;
CC topology: Linear;

12324359
 2 (bases 1 to 127923)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Submitted (19-APR-2002) Submitted on behalf of the pBtoxis
 sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
 Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
 Notes:
 Details of pBtoxis sequencing at the Sanger Centre are available on
 the World Wide Web.
 (URL, http://www.sanger.ac.uk/Projects/B_thuringiensis/).
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 Bh364 protein TR:Q9KAC5 (EMBL:AF001515) (378 aa) fasta
 scores: E(): 1.6e-18, 35.45% id in 189 aa, and weakly to
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 28.88% id in 90 aa, and to Bacillus thuringiensis
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 TR:Q49185 (EMBL:X53635) (254 aa) fasta scores: E():
 1.1e-37, 48.05% id in 231 aa"
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 4.2e-56, 84.15% id in 183 aa, and to Bacillus halodurans
 Bh364 protein TR:Q9KAC5 (EMBL:AF001515) (378 aa) fasta
 scores: E(): 1.6e-18, 35.45% id in 189 aa, and weakly to
 Lactobacillus delbrueckii integrase/recombinase orf2
 TR:Q48538 (EMBL:Z50864) (333 aa) fasta scores: E(): 6.3,
 28.88% id in 90 aa, and to Bacillus thuringiensis
 resolvase tnpI SW:TNRI BACTU (P10020) (284 aa) fasta
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RESULT 10
BTH251977
LOCUS   BTH251977
DEFINITION Bacillus thuringiensis subsp. medellin cry29Aa gene for Cry29Aa protein.
ACCESSION AJ251977
VERSION 1
KEYWORDS cry29Aa gene; Cry29Aa protein.
SOURCE    Bacillus thuringiensis serovar medellin
ORGANISM  Bacillus thuringiensis serovar medellin
          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
AUTHORS  Delecluse, A. and Orduz, S.
TITLE    Characterization of two new mosquitocidal toxins, Cry29A and Cry30A, from Bacillus thuringiensis medellin
JOURNAL  Unpublished
REFERENCE
AUTHORS  Delecluse, A.
TITLE    Direct Submission
JOURNAL  Submitted (22-DEC-1999) Delecluse A., Bacteries & Champignons Entomopathogenes, Institut Pasteur, 25, rue du Dr Roux, 75724 Paris Cedex 15, FRANCE

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Query Match 10.6%; Score 221.8; DB 1; Length 6009;
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Matches 376; Conservative 0; Mismatches 192; Indels 9; Gaps 3;

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RESULT 11
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DEFINITION Bacillus thuringiensis strain LDC-9 cry4A insecticidal protein (cry4A) gene, partial cds.
ACCESSION DQ078744
VERSION 1
KEYWORDS DQ078744.1 GI:68348788
SOURCE    Bacillus thuringiensis
ORGANISM  Bacillus thuringiensis
          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 434)
AUTHORS  Mahalakshmi, A., Sujatha, K. and Shenbagarathai, R.
TITLE    PCR analysis and molecular characterization of cry4A gene of indigenous Bacillus thuringiensis LDC-9
JOURNAL  Unpublished
REFERENCE 2 (bases 1 to 434)
AUTHORS  Mahalakshmi, A., Sujatha, K. and Shenbagarathai, R.
TITLE    Direct Submission
JOURNAL  Submitted (31-MAY-2005) PG Department of Zoology and Research Centre, Lady Doak College, Chinnachockikulam, Madurai, Tamilnadu 625002, India

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JOURNAL
FEATURES
source

AB125059 3752 bp DNA linear BCT 28-OCT-2003
Bacillus thuringiensis serovar entomocidus cry30Aa like gene for
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complete cdb.
AB125059
AB125059.1 GI:37999233
Bacillus thuringiensis serovar entomocidus
Bacillus thuringiensis serovar entomocidus
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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1
Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Bando, H. and Asano, S.
Cloning and Expression of Novel Crystall Protein Genes from Bacillus
thuringiensis subsp. entomocidus INA288
Unpublished
2 (bases 1 to 3752)
Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Asano, S. and Bando, H.
Direct Submission
Submitted (24-OCT-2003) Tomonori Ikeya, Graduate School of
Agriculture, Hokkaido University, Department of Applied Bioscience,
Kita-9-jo, Nishi-9-chome, Kita-ku, Sapporo, Hokkaido 0608589, Japan
(E-mail: ikeyan@ab.s.agr.hokudai.ac.jp, Tel:81-011-706-2487(ex.2487),
Fax:81-011-706-2487)

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DB 701 CTCGGTTTGGGGTTCAAAAGACTATTATGAATCTTTTAAAGAAAGAAATAGAGAGATATA 760
QY 680 GTAACCTATTGTCAAATACCTATAGAGAGAGCTAAATAAATCTTCCAAACGAACTTAATA 739
DB 761 CTAAATTTGTGCAGAAAACATATAGAAAACAGTTTAAATATATCTCAAAAACAAACCAATA 820
QY 740 TGAGATGGAGTATATTAAATGATTATCGAAGATATATGACTATTAATCTGATTATAGATACTA 799
DB 821 TCTCCTGGGATAGCTATAATAATATCGTAGAGAGCGACTTTAGGTGCATTAGATTAG 880
QY 800 TCGCTCAAATTTCTTTTATGATATAAAGAGATACAAAGATTCAAATAGGAAGATAGGTG 859
DB 881 TTGCATTATTCCCAAAATTAGCATATCGTAGAGAGCGACTTTAGGTGCATTAGATTAG 940
QY 860 GCATTAAACTGAATTTACAAGAGAAATTTATACAACTGAAATATAATTTTGACCGCTTA 919
DB 941 CTAGAAAAATTTATATGCGCATCATCGGTTTACAACTGAACTACTTCAAGTCTAG 1000
QY 920 CTTTACCTTGAATTCACCCCAATCTCGCTATATATGAATATAATTTAAACAGCTTCAGGCG 979
DB 1001 AAGGGTTAGAAAACGCACTTACGCATCCGCCATCATTTATTACTT-----GGTT 1049
QY 980 TTAGATTATTTTCATTTTATAGTGAATTTATTTTATACAAAATGAAACGTACGGGA 1039
DB 1050 AAAACGAATTAACCTTTATACAGTACGTGAAAATTTCAATCCAGCTTTTACAGGTATCTTC 1109
QY 1040 ATCGTTTAGTGTGTTTGGCAATCGTAATAGATCTACTTATGCTACGACAGGAACGTAAA 1099
DB 1110 ATTGCTGGTCTTCAAGCTAGATCTCGTTATACCCA-AAATCCAACTATCTTGATAATC 1168
QY 1100 TTATATATGGAGAAAGAACAGGTCCACCCCAACAAACAACTTTTAAATACCATTTGAATCCT 1159
DB 1169 CGGCTCAAGGAGTCAGAAATGGTACATCAACACAAATAGGTTTAAATAACTTGTGTTGTTT 1228
QY 1160 ATAAAGTTCAATTTGTAACGTGATAGACAGTAAGTACTCTACTTCCCTTTCCTTAACATAT 1219

DB 1229 ATAAATTAATCAATGTCACAAATATCATCATCAAAATGATTGTAGCTCAATAGCTGGATTT 1288
QY 1220 ACTTTTCAATTAATCAAAATGAACTTTATTTAAATAATTTCACTAGTAATAATAATTAACAT 1279
DB 1289 CGGATATGACCTTTTATAAAAGTGATTATAATGTTAAATGTCATCGGCAACTCA---AACTT 1345
QY 1280 ATTGAGCTGGGGGAATTTATCTAATGATAAAACAACTGATTTTCAATTTCCCTGTAA 1339
DB 1346 ATCAAGCAGGTAGAAACACAAATAATATGTCATAAATACA-----TTTGAATGGTCCAC 1399
QY 1340 AAAAGACTGTAAACCAATATTATTAATCCAAATTTGTTTACCAAGCTATAATAGTTATAGTC 1399
DB 1400 AAAAGACTCAAGCTCAATATATTTCCATTAACAAACAAAGCATATACTATCTGATA 1459
QY 1400 ATATTTTATCCAGTTTTCTTTTATTAATTTATTCCTATAAAATTTGATTTAGCGCTAAATA 1459
DB 1460 TTA-----AAATGATATATTTTCGAACCTGCGGAAATGTACCAAGTAT 1501
QY 1460 TATTATATACAGGTGCATTTAGGATGCACACAGTAGTGTAAATAGATAATAATGCAATAT 1519
DB 1502 ATGATTTTGGATATTTCATTTGCTCGACACATACATAGTGTAGATCTCTGATATATCTAATTG 1561
QY 1520 CAGATAAAATAATTAACAATGATCCAGCAATCAAAAGGTAAACAGTCTTTGTATACAAACTCTA 1579
DB 1562 TTCCAATATAGATTAACAAATCTCTGCTGTAAAGCTTTGGGAATCAGTACGGATTCAA 1621
QY 1580 AGGTAATTTGAAGGACCTGCTGCATACAGGAGGAACTTGGTTTATTTTAAAGTCAAGGGC 1639
DB 1622 AAGTTGTGAAGGACCTGTTTTTATAGGAGGAGATTTACTCCTTCTGAAAATTTACAAG--- 1678
QY 1640 GTTTAGATTTACATGTAGAACTCCCTTAATTTCTACACAATCTTTATTTACATTTAGACTTCGAT 1699
DB 1679 ---CAACCATTTAGAAATTAACACAGATCACGCTAAACATCGTTTATAAAATACGTTTCGAT 1735
QY 1700 AGCTTACAAATCGTCTCGAAATATCTCTCTTAATATATCTCTTACAAATACCAGGAGTAA 1759
DB 1736 ATGCTTCCATG-----CAATACACCAATAGTGTATCATCATAC 1777
QY 1760 TAGGAATACCCTCAACGACTCAACACACTTTTTCTGGTACAAATTAATAATAATTATAC 1819
DB 1778 AAAATACATTAACAGTTAGCTTTCCACAACTATAAATCAATCACTATTAGCGAGTTAC 1837
QY 1820 AATACGGAGATTTTGGGTATTTCCAAATTTCCAAATGACAGTACATTTACCTTTAAATCGAA 1879
DB 1838 AATATAAAGATTTTCAATATGTAACATTTCCCAAGGTGAATTTATAATGGAT---AAGCCAA 1894
QY 1880 ACATACCAATTTATATTATTTAATCGTCAGATGATCAAAATTTCAATTTTAAATCATTTGATAAA 1939
DB 1895 GTATAGATGTAGCTATAGAGGTGTACAAATGATCGCAATGATATATGATAGATAGAA 1954
QY 1940 TTGAATTTATACCAATTTACTTCTCTGTACGCCAAATAGAGAAACAAACAAATTTAGAA 1999
DB 1955 TTGAATTTCTTCCAATTAATCAATCTGTATTAGATTTATACAGAGGAACAAACATAGAA 2014
QY 2000 CTATCCAAACAAATAATTAATCAATTTTTCACAAATCATACAAA 2043
DB 2015 AATCACAGAAAGCGGTGAATGACCTTTTATCAATTTAAACAAA 2058

RESULT 14

AB193814
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE

AB193814 3642 bp DNA linear BCT 28-OCT-2004
Bacillus thuringiensis gene for Cry30-like, hypothetical protein,
complete cds.
AB193814
AB193814.1 GI:54695304
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1

1718	Db	GTAGCTTTACTGGAGCTTCCAGACGTTATGGTATACGCATACGTTATGCTGCAAAATAATG	1777
1715	Qy	CTGGAATACTCTCCCTAAATATATATCTCTTACAAATACCAGAGTAATAGGAATACCACTTC	1774
1778	Db	C-ATTGACAGTGAGTCTATCATATACGTGACAA--GGTGGGAATACAAATAGTAGTACAACATT	1835
1775	Qy	AACGACTCAACAACACACTTTTT-----CTGGTACAAATTTATAATAAATTTACAATACGG	1826
1836	Db	TATTACCGAAGGTACATTTTTTAAGACCTAATATATACAATACCAACGGATTTAAATACGA	1895
1827	Qy	AGATTTTGGGTATTTCCTAAATTTCCAAGTACAGATAACTACCTTTAAATCGAAACATACC	1886
1896	Db	GGAGTTTAAATATAAAGAAATATAATCAAAATTATTACAATGACTGCACCCCAAAATACAAT	1955
1887	Qy	ATT-----TATATTTAATCGTGAGATGTACAAATTCAAATTTCAATTTAATCAATTGTATAA	1937
1956	Db	AGTAACTATAGCTATCCAAACAACTAAATGGTTTCCAAATGATCAATTAATTTATGTATAG	2015
1938	Qy	AATTGAATTTATACCAAATTACTTCTCTGTACGCCAAAATAGAGAAAACAAAAATTTAGA	1997
2016	Db	AATCGAATTTTATCCAAATGGATCAAGGTGTAGTACCTTTGTACAGTAAACTAAAGATTAGA	2075
1998	Qy	AACATATCCAAACAAAAATAAATACATTTTTTCCAAATCATACAAAA	2043
2076	Db	AAAATCAAAAAAAGAGTTAATATCTATTTTATTAGTTTAAACAAA	2121

RESULT 15
AF132928 4896 bp DNA linear BCT 14-JAN-2000
LOCUS AF132928
DEFINITION *Bacillus thuringiensis* subsp. *finitimus* Cry28Aa1 delta-endotoxin
gene, complete cds.
ACCESSION AF132928
VERSION AF132928.1 GI:4574729
KEYWORDS
SOURCE *Bacillus thuringiensis* serovar *finitimus*
ORGANISM *Bacillus thuringiensis* serovar *finitimus*
Bacteria; *Firmicutes*; *Bacillales*; *Bacillaceae*; *Bacillus*
cereus group.
REFERENCE 1 (bases 1 to 4896)
AUTHORS Wojciechowska, J.A., Lewitin, E., Revina, L.P., Zalunin, I.A. and
Chestukhina, G.G.
TITLE Two novel delta-endotoxin gene families cry26 and cry28 from
Bacillus thuringiensis spp. *finitimus*
JOURNAL PDBS Lett. 453 (1-2), 46-48 (1999)
PUBMED 10403372
REFERENCE 2 (bases 1 to 4896)
AUTHORS Wojciechowska, J.A., Lewitin, E.I. and Chestukhina, G.G.
TITLE Direct Submission
JOURNAL Submitted (04-MAR-1999) Laboratory of Protein Chemistry, Institute
of Microbial Genetics, Dorozhny proezd, Moscow 113545, Russia
LOCATION/Qualifiers
FEATURES

CDS

SVNSQNLSIESVSQTQIPLVKAIVEYTNNSVIRGPGTGGDLIELRDKCSIKCKRASSILK
YAIISFYAANNAIVSDVSGAGVLQIOPFRKGNNTFIQDLNLYQFOFQVHTLLVD
LELPSEBIEHTHLKREDSYEGVILIDKLFQFPIDENYTNENNELKAKKANVNLIN
ATNALKMDVTDHIDQANVLVECTSDIYAKELIKFTFCPEKQSQARNLSLSDNF
NLNAEWSWTANGTIIIEGDP LKGRALISAAARENDPVTLYQKIDSLKLPYTRY
OLRCFVSGSDLELDLVRYGATDIWMNVPGDLIELISYAPINPCBEIEHTLTCGAL
DRQKQSYNSAADVREPQVNGDPEAFSHDITGCTDNNRNLGIIWIFKIANPDGYAT
FGNUELIELPGSEALQVQKEQKQWGNNTQKREBAKULYAAKQOTINQLFPADSQG
TKLRFDPTEFNLSADKLAVYKIRDVYBSVPLGNDYDLFMFENELQNALDLYDAR
NTVTNGFGRNGLANMASSNTEVRQIQHPQWISYGLWNAQSLNVRKDPGYLVYAR
AKKEGIGNGYVTILDCAHNHITLTFSSCDSGFTSSNELAAVYTKLEIFPPTDQIRI
RIGETRTSEYVESVYDILTMRYH"

ORIGIN

Query Match	7.7%	Score 161.2	DB 1	Length 4896
Best Local Similarity	57.0%	Pred. No. 9.3e-13		
Matches 385	Conservative 0	Mismatches 243	Indels 48	Gaps 3
Qy	153	AGGTGCTATAAATAATCTCTTTGGTACCCCTAATCACTGCTCTTTGGCCGCGGAGAACCA	212	
Db	1293	AGGTGGTGACTTATATCATCAATTTTGGAAACCTTGGCTCCGTTCTTTGGCCTGATCCAGGGA	1352	
Qy	213	AGA---CAAAAACAGTATGACACAAATTTATTAATAATGGGAGAAATTTTTTGTGTGATACACC	269	
Db	1353	AGATCCAAAAAAAATTTGGTCACAAATTTATGAACACGCGAGAAGACCTTTTAATCAAAAC	1412	
Qy	270	GTTTACAGAAAGCATATAAACACAGCTAAGTTTACAACTTTAGAGGAATTTAGACAAATATT	329	
Db	1413	AATTTCTACAGCTGTAAAAAGAAATAGCATAGCTCATCTTAAATGGTTTAAAGATGTATT	1472	
Qy	330	ACAAAGCTATATACAGCATTTAGATGATTTGGAGAAATTTAAAAAGACTACAAAGCTCCTGG	389	
Db	1473	AAGTACTATGAAGAGCAATTTAATGATTTGGAGAGAAATCCAAAGTGCAAAATACTGCCAG	1532	
Qy	390	ATTACCAACCATCATCAGCATTTACAACAGCTGCCTTGACTCTTAAAAATACGATTTGAGAA	449	
Db	1533	ATTGGTATCACAGA-----GATTTGAAAA	1556	
Qy	450	TGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACGCT	509	
Db	1557	CGTCAATTTCAAATTTTGTGAAGCAATATGCAACAACTTCCAACTTCCACGCTATGACACATT	1616	
Qy	510	ATTACTACCTATTATAGCCGACAGCTGCTAAATTTTCATTTAAATTTATTAACAACAGAGTGC	569	
Db	1617	ATTATTAAGTTGCTATACAGAAGCTGCAAAATTTTACATTTTGAATTTATTAATCAAGGTGT	1576	
Qy	570	TGAATTTGGCTGATGAATGGAATGCAGATATACATCTTCCAAAATTTGAACCTAATGCTGG	639	
Db	1677	ACAAATTCGGGATCAATGGAATGCAGATCAACACATTCACCAAT-----GTTGAA	1727	
Qy	630	AACATCAGATGACTATTATAAATTTTAAAGAAATATACCTAAATATAGTAACCTATTG	689	
Db	1728	GTCAATCAGGTACTTATTATGACGAGCTATTGGTATATATTGAAAAGTATATTAAATTTATTG	1787	
Qy	690	TGCBAATACCTATAGAGAAGGACTAAATAAACTTCGAAAACGAACTTAATATGAGATGGAG	749	
Db	1788	CACCAAGACATACCAATAAAGGATTTGAATCACCTTTAAGAAATCAGAAAAAATCATCTGGGA	1847	
Qy	750	TATATTTAATGATTCGAAGATATATGACTATTACTGTATTAGATACCTATCGCTCAATT	809	
Db	1848	TGCTTATACACATATCGTCGAGAAATGACCTTAATTTGATTGGATCTTGTGCGCAACTTT	1907	
Qy	810	TTCTTTTATGATATA	825	
Db	1908	TCCTTTTATGATATA	1923	

Search completed: February 15, 2006, 03:24:50
Job time : 10541 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	2085	100.0	2085	13	ADR89398	Adr89398 AXMI-007
2	2085	100.0	2235	13	ADR89396	Adr89396 AXMI-007
3	1794.4	86.1	2208	13	ADR89394	Adr89394 AXMI-006
4	334.6	16.0	3940	1	AAN93054	Aan93054 Delta-end
5	334.6	16.0	4571	1	AAN93059	Aan93059 Delta-end
6	334.6	16.0	4934	1	AAN91490	Aan81490 Insectici
7	331.4	15.9	3543	2	AAQ14669	AAQ14669 Dipteran
8	331.4	15.9	3543	2	AAQ81178	AAQ81178 B.t. toxi
9	161.2	7.7	4896	6	AA43974	AA43974 Bacillus
10	161.2	7.7	4896	10	ADP31301	Adf31301 Bacillus
11	161.2	7.7	4896	10	ADP31306	Adf31306 Bacillus
12	158	7.6	2061	2	AAQ14670	AAQ14670 Dipteran
13	158	7.6	2061	2	AAQ81180	AAQ81180 B.t. toxi
14	148.2	7.1	3756	6	AAN50525	Aan50525 Bacillus
15	117	5.6	15548	6	ABL34155	Abt34155 Human Imm
16	101.2	4.9	3684	1	AAK82106	Aak82106 Sequence
17	101	4.8	3684	6	AAK14949	Abk14949 Bacillus
18	100.6	4.8	3535	1	AAN91003	Aean91003 Sequence
19	100.6	4.8	3684	14	AEA61392	Aea61392 Bacillus

XX Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
DR P-PSDB; ADR89399.
XX
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
PS Claim 1; SEQ ID NO 10; 178pp; English.
XX
CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
SQ Sequence 2085 BP; 794 A; 338 C; 302 G; 651 T; 0 U; 0 Other;
Query Match 100.0%; Score 2085; DB 13; Length 2085;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2085; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTCAGGGAATACAAATATGTGATATTTTCAGACATTTTCTAGTGTGTATACA 60
DB 1 ATGTGTCAGGGAATACAAATATGTGATATTTTCAGACATTTTCTAGTGTGTATACA 60
QY 61 ATTGTGTCAGTGTAGTGCAGGTACTATTGTATCGGTACTCTGTAGCCGGTATAGTGGG 120
DB 61 ATTGTGTCAGTGTAGTGCAGGTACTATTGTATCGGTACTCTGTAGCCGGTATAGTGGG 120
QY 121 CTCACCTTCTATATCCGACCGATAGGAATATAGGTGCTATATATATCTTTTGGTACC 180
DB 121 CTCACCTTCTATATCCGACCGATAGGAATATAGGTGCTATATATATCTTTTGGTACC 180
QY 181 CTAATCACTGTCTTTTGGCCCGGGAGAACAGACAAACAGATGGAACAATTTATT 240
DB 181 CTAATCACTGTCTTTTGGCCCGGGAGAACAGACAAACAGATGGAACAATTTATT 240
QY 241 AAAATGGGAGAAATTTTGTGTGATACACCGTTAAACAGAAAGCATAAACAGCTAAAGTTA 300
DB 241 AAAATGGGAGAAATTTTGTGTGATACACCGTTAAACAGAAAGCATAAACAGCTAAAGTTA 300
QY 301 CAAACTTTAGAGGATTTAGACAAATTTTACAAAGCTATAATACAGCATTAGATGATGG 360
DB 301 CAAACTTTAGAGGATTTAGACAAATTTTACAAAGCTATAATACAGCATTAGATGATGG 360
QY 361 AGAAATTTAAAGACTACAAGCTCCTGGATTACCAACCATCATCAGCATTAACAACAGCT 420
DB 361 AGAAATTTAAAGACTACAAGCTCCTGGATTACCAACCATCATCAGCATTAACAACAGCT 420
QY 421 GCCTTGACTCTTAAAAATACGATTTGAGATGTTTCAAAATGATTTTATTCGAGAAATACCT 480
DB 421 GCCTTGACTCTTAAAAATACGATTTGAGATGTTTCAAAATGATTTTATTCGAGAAATACCT 480
QY 481 GGTTCCTCACTTGAACCTTATAAAGCTATTACTACCTATTATTCGGCAAGCTGCTAAT 540
DB 481 GGTTCCTCACTTGAACCTTATAAAGCTATTACTACCTATTATTCGGCAAGCTGCTAAT 540
QY 541 TTTTCATTTAAATTTATTACAAAGGTGCTGAATTTGGCTGATGAATGGAATGCAGATATA 600
DB 541 TTTTCATTTAAATTTATTACAAAGGTGCTGAATTTGGCTGATGAATGGAATGCAGATATA 600

QY 601 CATCTTTCACAAATTGAACCTAATGCTGGAAACATCAGATGACTATTATATAAATCTTTTAAAA 660
DB 601 CATCTTTCACAAATTGAACCTAATGCTGGAAACATCAGATGACTATTATATAAATCTTTTAAAA 660
QY 661 GAAAAATATACCTTAAATATAGTAACTATTGTGCAAAATACCTATAGAGAAGGACTTAAATAA 720
DB 661 GAAAAATATACCTTAAATATAGTAACTATTGTGCAAAATACCTATAGAGAAGGACTTAAATAA 720
QY 721 CTTTCAAGAACCACTTAAATATAGATGGAGTATATTTTAAATGATTTATCGAAGATATATGACT 780
DB 721 CTTTCAAGAACCACTTAAATATAGATGGAGTATATTTTAAATGATTTATCGAAGATATATGACT 780
QY 781 ATTACTGTATTAGATACCTATCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGAT 840
DB 781 ATTACTGTATTAGATACCTATCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGAT 840
QY 841 TCAATAGGAAGAATAGGTGGCAATTAAAACTGAACTTCAAGAGAAATTTATACAACCTGAA 900
DB 841 TCAATAGGAAGAATAGGTGGCAATTAAAACTGAACTTCAAGAGAAATTTATACAACCTGAA 900
QY 901 ATAAATTTTGACCGTCTTACTTACCTTGAATTTCAACCCNAATCTCGCTATAATGGAATAT 960
DB 901 ATAAATTTTGACCGTCTTACTTACCTTGAATTTCAACCCNAATCTCGCTATAATGGAATAT 960
QY 961 AATTTTAAACAGTTCAGGCGCTTAGATATTCTTCAATTTTAGATGAACTTATATTTTATACA 1020
DB 961 AATTTTAAACAGTTCAGGCGCTTAGATATTCTTCAATTTTAGATGAACTTATATTTTATACA 1020
QY 1021 AAAAAATGAACGTACGGGAATCGTTTAGTGTGATTTGCGNAATCGTAATAGATCTACTTAT 1080
DB 1021 AAAAAATGAACGTACGGGAATCGTTTAGTGTGATTTGCGNAATCGTAATAGATCTACTTAT 1080
QY 1081 GCTACGACAGGAACTGAAATTTATATATGAGAGAAAGACAGGTCACCCCAACAAAAAATCT 1140
DB 1081 GCTACGACAGGAACTGAAATTTATATATGAGAGAAAGACAGGTCACCCCAACAAAAAATCT 1140
QY 1141 TTAATACCAATTTGAATCCTATAAAGTTTCAATTTGTAACCTGATAGACAAGTAACTCTACT 1200
DB 1141 TTAATACCAATTTGAATCCTATAAAGTTTCAATTTGTAACCTGATAGACAAGTAACTCTACT 1200
QY 1201 TCCCTCTTTTCTTAAACATATACCTTTTCAATTAATCAAAATTTGAACCTTTTAAATAATTTCA 1260
DB 1201 TCCCTCTTTTCTTAAACATATACCTTTTCAATTAATCAAAATTTGAACCTTTTAAATAATTTCA 1260
QY 1261 CCTAGTAATAAATTAACATATTCAGCTGGGGGGAATTTATCTTAATGATTAATAAACAACACT 1320
DB 1261 CCTAGTAATAAATTAACATATTCAGCTGGGGGGAATTTATCTTAATGATTAATAAACAACACT 1320
QY 1321 GATTTTCAATTTCTGTAAAAAAGACTGTAAACCAATTTATTAAATCCAAATTTGTTTACCA 1380
DB 1321 GATTTTCAATTTCTGTAAAAAAGACTGTAAACCAATTTATTAAATCCAAATTTGTTTACCA 1380
QY 1381 AGCTATAATAGTATTAGTCATATTTTATCCCAAGTTTCTTTTATTTTAAATTTTCTTATAAA 1440
DB 1381 AGCTATAATAGTATTAGTCATATTTTATCCCAAGTTTCTTTTATTTTAAATTTTCTTATAAA 1440
QY 1441 ATTGGAATAGCGCTAAATATATTTATATACAGTGCAATTAGGATGGACACACAGTAGTGT 1500
DB 1441 ATTGGAATAGCGCTAAATATATTTATATACAGTGCAATTAGGATGGACACACAGTAGTGT 1500
QY 1501 AATAGAAATATGCAATATCAGATAAATAATTAACAATGATCCCAAGCAATCAAGAGTAAC 1560
DB 1501 AATAGAAATATGCAATATCAGATAAATAATTAACAATGATCCCAAGCAATCAAGAGTAAC 1560
QY 1561 AGTCTTTGATACAAACTCTAAGGTAAATTTGAAGGACCTGGTCTATACAGGAGGAACTTGGTT 1620
DB 1561 AGTCTTTGATACAAACTCTAAGGTAAATTTGAAGGACCTGGTCTATACAGGAGGAACTTGGTT 1620
QY 1621 TATTTTCAAAAGTCAAGGGGTTTAGAGATTAATGATAGAACTCTCTAAATTTCTTACAAATCT 1680
DB 1621 TATTTTCAAAAGTCAAGGGGTTTAGAGATTAATGATAGAACTCTCTAAATTTCTTACAAATCT 1680
QY 1681 TATTACATTAGACTTCGATACGCTACAAATGGTGTGGAAATACTCTTCTCTTAATATATCT 1740

1681 TATTACATTAGACTTCGATACGCTACAAATGGGCTGGAAATACTCTTCTTAATATCT 1740
1741 CTTTACAAATACAGGAGTAATAGGAATACCACTCAACGACTCAACACACTTTTCTGGT 1800
1741 CTTTACAAATACAGGAGTAATAGGAATACCACTCAACGACTCAACACACTTTTCTGGT 1800
1801 ACAAATTAATTAATTTACAAATACGAGATTTGGGTATTTCCAAATTTCCAAGTACAGTA 1860
1801 ACAAATTAATTAATTTACAAATACGAGATTTGGGTATTTCCAAATTTCCAAGTACAGTA 1860
1861 ACATTACCTTTAAATCGAAATACCACTTTATTTAAATCGTGAGATGTATCAAAATCA 1920
1861 ACATTACCTTTAAATCGAAATACCACTTTATTTAAATCGTGAGATGTATCAAAATCA 1920
1921 ATTTTATCATTTGATAAAATTTGAATTTATACCAATTAATCTCTCTGTACGCCAAATAGA 1980
1921 ATTTTATCATTTGATAAAATTTGAATTTATACCAATTAATCTCTCTGTACGCCAAATAGA 1980
1981 GAAAAACAAAAATTTAGAACTATCCAAACAAAAATTAATATATTTTTCACAAATCATACA 2040
1981 GAAAAACAAAAATTTAGAACTATCCAAACAAAAATTAATATATTTTTCACAAATCATACA 2040
2041 AAAAAATCTTTAAATATAGAGCCACAACTATCATATTTGATTA 2085
2041 AAAAAATCTTTAAATATAGAGCCACAACTATCATATTTGATTA 2085

RESULT 2
ADNR89396 standard; cDNA; 2235 BP.

ADNR89396;
18-NOV-2004 (first entry)
AXMI-007 coding sequence.

ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
expression cassette; transformation; transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
pesticidal activity.

Bacillus thuringiensis.

Key Location/Qualifiers
CDS 1..2235
FT /tag= a
FT /product= "AXMI-007"
FT /transl_except= pos:1..3, aa:Met

WO2004074462-A2.

02-SEP-2004.

20-FEB-2004; 2004WO-US005829.

20-FEB-2003; 2003US-0448632P.

20-FEB-2003; 2003US-0448633P.

20-FEB-2003; 2003US-0448797P.

20-FEB-2003; 2003US-0448806P.

20-FEB-2003; 2003US-0448810P.

20-FEB-2003; 2003US-0448812P.

19-FEB-2004; 2004US-00781979.

19-FEB-2004; 2004US-00782020.

19-FEB-2004; 2004US-00782096.

19-FEB-2004; 2004US-00782141.

19-FEB-2004; 2004US-00782570.

19-FEB-2004; 2004US-00783417.

(ATHE-) ATHENIX CORP.

Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

XX WPI: 2004-635574/61.
DR P-PSDB; ADR89397.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.

XX Claim 1; SEQ ID NO 8; 178pp; English.

XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

XX SQ Sequence 2235 BP; 861 A; 364 C; 316 G; 694 T; 0 U; 0 Other;

Query Match 100.0%; Score 2085; DB 13; Length 2235;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2085; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTCAGGGAATACAAATATGGTGATAATTTTCGAGACATTTGCTAGTGTGATACA 60
Db 151 ATGTGTCAGGGAATACAAATATGGTGATAATTTTCGAGACATTTGCTAGTGTGATACA 210
Qy 61 ATTGCTCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTGTTAGCGGTATAGTGGG 120
Db 211 ATTGCTCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTGTTAGCGGTATAGTGGG 270
Qy 121 CTGACTCTATATCCGACCGATAGGAATATAGTGTCTATTAATTAATCTTTTGGTACC 180
Db 271 CTCATTTCTATATCCGACCGATAGGAATATAGTGTCTATTAATTAATCTTTTGGTACC 330
Qy 181 CTATCACTGTCTTTTCGCGGGAGAACAAACAGATATGATGACACAAATTTATT 240
Db 331 CTATCACTGTCTTTTCGCGGGAGAACAAACAGATATGATGACACAAATTTATT 390
Qy 241 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATAAAACAGCTAAAGTTA 300
Db 391 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATAAAACAGCTAAAGTTA 450
Qy 301 AAAATCTTTAGAGGATTTAGACAAATATTACAAAGCTATATATACAGCATTTAGATGATGG 360
Db 451 AAAATCTTTAGAGGATTTAGACAAATATTACAAAGCTATATATACAGCATTTAGATGATGG 510
Qy 361 AGAAATTTAAAGACATACAGCTCTGGATTACACCATCATCAGCATTTACCAAGCT 420
Db 511 AGAAATTTAAAGACATACAGCTCTGGATTACACCATCATCAGCATTTACCAAGCT 570
Qy 421 GCCTTGACTCTTAAAAATACGATTTGAGAAATGTTTCAATGATTTTATTCGAGAAATACCT 480
Db 571 GCCTTGACTCTTAAAAATACGATTTGAGAAATGTTTCAATGATTTTATTCGAGAAATACCT 630
Qy 481 GGTTCGAACTTGAAACTTATAAAACGCTATTACTACCTATTATTCGCGCAGCTGCTAAT 540
Db 631 GGTTCGAACTTGAAACTTATAAAACGCTATTACTACCTATTATTCGCGCAGCTGCTAAT 690
Qy 541 TTTTCATTTAAATTTATACAAAGGCTCGCAATGGCTGATGAATGAAATGCGAGATATA 600
Db 691 TTTTCATTTAAATTTATACAAAGGCTCGCAATGGCTGATGAATGAAATGCGAGATATA 750
Qy 601 CATCTTTCACAAATTTGAACCTTAATGCTGGAAATCATCAGATGATATTAATTAATTTAAAA 660

Db 751 CATCTTTCACAAATTGAACCTTAATGCTGGAAATCAGATGACTATTTATAAACTTTTAAAA 810
Qy 661 GAAATATATACCTAAATATATAGTAATCTATGTCAAATACCTATAGAGAGGACTTAAATAAA 720
Db 811 GAAATATATACCTAAATATATAGTAATCTATGTCAAATACCTATAGAGAGGACTTAAATAAA 870
Qy 721 CTTTGAAGAGAACTTAATATGAGATGGAGTATATTTAATGATATATCGAAGATATATGACT 780
Db 871 CTTTGAAGAGAACTTAATATGAGATGGAGTATATTTAATGATATATCGAAGATATATGACT 930
Qy 781 ATTACTGTATATAGATACCTACCTCAATTTCTTTTATGATATAAGAGATACAAAGAT 840
Db 931 ATTACTGTATATAGATACCTACCTCAATTTCTTTTATGATATAAGAGATACAAAGAT 990
Qy 841 TCAATAGGAAGAATAGGTGGCAATTAACCTGAACTTAACAAGAGAAATTTATACAACTGAA 900
Db 991 TCAATAGGAAGAATAGGTGGCAATTAACCTGAACTTAACAAGAGAAATTTATACAACTGAA 1050
Qy 901 ATAAATTTTGACCGTCTTACTTACCTTGAAATTCACCCCAATCTCGCTATATATGGAATAT 960
Db 1051 ATAAATTTTGACCGTCTTACTTACCTTGAAATTCACCCCAATCTCGCTATATATGGAATAT 1110
Qy 961 AATTTAACACGTTTCAGGCTTATAGATATTTTCAATTTTATAGATGAACCTTATATTTATACA 1020
Db 1111 AATTTAACACGTTTCAGGCTTATAGATATTTTCAATTTTATAGATGAACCTTATATTTATACA 1170
Qy 1021 AAAAAATGAACGTAACGGGAATCGTTAGTTGGTATTCGGAATCGTAAATAGATCTACTTAT 1080
Db 1171 AAAAAATGAACGTAACGGGAATCGTTAGTTGGTATTCGGAATCGTAAATAGATCTACTTAT 1230
Qy 1081 GCTACGACGAGGAACCTGAATATATATGAGAGAAAGACGGTCCACCCACACAAACCT 1140
Db 1231 GCTACGACGAGGAACCTGAATATATATGAGAGAAAGACGGTCCACCCACACAAACCT 1290
Qy 1141 TTAATACCAATTTGAATCCTATTAAGTTTCAATTTGTAACCTGATAGACAAAGTCTCTACT 1200
Db 1291 TTAATACCAATTTGAATCCTATTAAGTTTCAATTTGTAACCTGATAGACAAAGTCTCTACT 1350
Qy 1201 TCCCTTTTCTTAACATATACCTTTACAAATTAATCAAAATTTAAATTAATTAATCA 1260
Db 1351 TCCCTTTTCTTAACATATACCTTTACAAATTAATCAAAATTTAAATTAATTAATCA 1410
Qy 1261 CCTAGTAATTAATTAACATATTCAGCTGGGGGAATTTATCTAATGATAAAAAACAAT 1320
Db 1411 CCTAGTAATTAATTAACATATTCAGCTGGGGGAATTTATCTAATGATAAAAAACAAT 1470
Qy 1321 GATTTTCAATTTCTCTAATAAAGACCTGTAACCAATTAATTAATCAAAATTTGTTTACCA 1380
Db 1471 GATTTTCAATTTCTCTAATAAAGACCTGTAACCAATTAATTAATCAAAATTTGTTTACCA 1530
Qy 1381 AGCTATAATAGTTATAGTCAATTTTATCCAGTTTCTTTTATTTAATTTATTCCTATAAA 1440
Db 1531 AGCTATAATAGTTATAGTCAATTTTATCCAGTTTCTTTTATTTAATTTATTCCTATAAA 1590
Qy 1441 ATTGGATTAGCGCTAATATATATATACAGTGGCAATTAGGATGGACACACAGTAGTGTT 1500
Db 1591 ATTGGATTAGCGCTAATATATATATACAGTGGCAATTAGGATGGACACACAGTAGTGTT 1650
Qy 1501 AATAGAAATAATGCAATATCAGATAAATAATTAACAATGATCCAGCAATCAAAAGGTAAC 1560
Db 1651 AATAGAAATAATGCAATATCAGATAAATAATTAACAATGATCCAGCAATCAAAAGGTAAC 1710
Qy 1561 AGTCTTTGATACAAACTCTAAGGTAATTTGAAGGACCTGGTCATACAGGAGGAACTTGGTT 1620
Db 1711 AGTCTTTGATACAAACTCTAAGGTAATTTGAAGGACCTGGTCATACAGGAGGAACTTGGTT 1770
Qy 1621 TATTTACAAAGTCAGGGGTTTAGAGATTAATGATAGAACTCCTTAATTTCTACAAATCT 1680
Db 1771 TATTTACAAAGTCAGGGGTTTAGAGATTAATGATAGAACTCCTTAATTTCTACAAATCT 1830
Qy 1681 TATTACATTTAGACTTCGATACGCTACAAATGGTGGTGGAAATCTCTTCTAATATATCT 1740
Db 1831 TATTACATTTAGACTTCGATACGCTACAAATGGTGGTGGAAATCTCTTCTAATATATCT 1890

Qy 1741 CTTACAATACCAAGGAGTATAGGAATACCACTCAACGACTCAACAACCTTTTCTGGT 1800
Db 1891 CTTACAATACCAAGGAGTATAGGAATACCACTCAACGACTCAACAACCTTTTCTGGT 1950
Qy 1801 ACAAAATTAATAAATTTACAATACGAGATTTTGGGTATTTCCAAATTTCCAAAGTACAGTA 1860
Db 1951 ACAAAATTAATAAATTTACAATACGAGATTTTGGGTATTTCCAAATTTCCAAAGTACAGTA 2010
Qy 1861 ACATTACCTTTTAAATCGAAACATACCAATTTATTTAATTCGTGCGAGATGATCAAAATTC 1920
Db 2011 ACATTACCTTTTAAATCGAAACATACCAATTTATTTAATTCGTGCGAGATGATCAAAATTC 2070
Qy 1921 ATTTTAATCATTTGATATAAATTTGAATTTATACCAATTTACTTCTCTGTACGCCAAAATAGA 1980
Db 2071 ATTTTAATCATTTGATATAAATTTGAATTTATACCAATTTACTTCTCTGTACGCCAAAATAGA 2130
Qy 1981 GAAAAACAAAATTTAGAACTATCCAAAACAAAATAAATAFACATTTTTCACAAATCATACA 2040
Db 2131 GAAAAACAAAATTTAGAACTATCCAAAACAAAATAAATAFACATTTTTCACAAATCATACA 2190
Qy 2041 AAAAAATACCTTTAAATATATAGAACCCCAAACTATGATATTGATTAA 2085
Db 2191 AAAAAATACCTTTAAATATATAGAACCCCAAACTATGATATTGATTAA 2235
RESULT 3
ADR89394
ID ADR89394 standard; cdna; 2208 BP.
XX
AC ADR89394;
XX
DT 18-NOV-2004 (first entry)
XX
DE AXMI-006 coding sequence.
XX
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 1..2208
FT /*tag= a
FT /product= "AXMI-006"
XX
PN WO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
PI Carozzi N, Hargiss T, Kozziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
DR P-PSDB; ADR89395.
DR

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
XX
PS Claim 1; SEQ ID NO 6; 178pp; English.
XX
CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
SQ Sequence 2208 BP; 842 A; 377 C; 308 G; 681 T; 0 U; 0 Other;
Query Match 86.1%; Score 1794.4; DB 13; Length 2208;
Best Local Similarity 92.7%; Pred. No. 3.9e-290;
Matches 1908; Conservative 0; Mismatches 141; Indels 9; Gaps 2;
QY 1 ATGTGTCAGGGAATACACAATATGGTGATAATTTTCGAGACATTTGCTAGTGTGATACA 60
DB 154 ATGTGTCAGGGAATACACAATATGGTGATAATTTTCGAGACATTTGCTAGTGTGATACA 213
QY 61 ATGTGTCAGTGTAGTCAGTACTATTGTATCCGGTACTCTGTAGCCGGTATAGTGGG 120
DB 214 ATGTGTCAGTGTAGTCAGTACTATTGTATCCGGTACTCTGTAGCCGGTATAGTGGG 273
QY 121 CTGACTTCTATATCCGACCGATAGGAATATAGGTGCTATAATATCTTTTGGTACC 180
DB 274 CTCACCTTCTATATCCGACCGATAGGAATATAGGTGCTATAATATCTTTTGGTACC 333
QY 181 CTATCACTGTCTTTTGGCCGGGAGAACAGACAAAACAGTATGGACACAAATTTATT 240
DB 334 CTATCACTGTCTTTTGGCCGGGAGAACAGACAAAACAGTATGGACACAAATTTATT 393
QY 241 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATAAAACAGCTAAAGTTA 300
DB 394 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATAAAACAGCTAAAGTTA 453
QY 301 CAAACTTTAGAGGATTTAGACAAATATTACAAAGCTATATACAGCATTTAGATGATGG 360
DB 454 CAAACTTTAGAGGATTTAGACAAATATTACAAAGCTATATACAGCATTTAGATGATGG 513
QY 361 AGAAAAATTAAGACATACAGCTCTCGATTACCAACATCATCAGCATTTACAAACAGCT 420
DB 514 AGAAAAATTAAGACATACAGCTCTCGATTACCAACATCATCAGCATTTACAAACAGCT 573
QY 421 GCCTTTGACTCTTAAATAACGATTTGAGAAATGTTTCAATGATTTTATTCGAGAAATACCT 480
DB 574 GCCTTTGACTCTTAAATAACGATTTGAGAAATGTTTCAATGATTTTATTCGAGAAATACCT 633
QY 481 GGTTCGAACTTGAACTTATAAACGCTATTACTACTATTATTCGCAAGCTGCTTAAT 540
DB 634 GGTTCGAACTTGAACTTATAAACGCTATTACTACTATTATTCGCAAGCTGCTTAAT 693
QY 541 TTTTCATTTAAATTTATTACAAAGGCTGCTGAAATTTGGCTGATGAATGGAATGCGAGATATA 600
DB 694 TTTTCATTTAAATTTATTACAAAGGCTGCTGAAATTTGGCTGATGAATGGAATGCGAGATATA 753
QY 601 CATCTTTCACAAATGAACTTAATGCTGGAAACATCAGATGATATTAATACTTTTAAAA 660
DB 754 CATCTTTCACAAATGAACTTAATGCTGGAAACATCAGATGATATTAATACTTTTAAAA 813
QY 661 GAAAAATATACCTAAATATAGTAACTATTGTGCAAAATACCTATAGAGAAGGACTAAATAAA 720

DB 814 GAAAAATATACCTAAATATAGTAACTATTGTGCAAAATACCTATAGAACAGGACTTAAAAAT 873
QY 721 CTTTGAAGACCACTTAATATAGATGGAGTATATTTAATGATTATTCGAAGATATATGACT 780
DB 874 CTTAGAGACGAACCAATATGAATGGAGTATATTTAATGACTATTCGAAGATATATGACC 933
QY 781 ATTACTGTATATAGACTATCGCTCAATTTCTTTTATGATATATAAGAGATACAAAGAT 840
DB 934 ATTACTGTATATAGATACCATCTCTCAATTTCTTTATATGATATAAAAGATATAGAGAT 993
QY 841 TCAATAGGAAAGATAG-----GTGGCATTAACCTGAACCTTACAAGAGAAATTTATACA 894
DB 994 TCAATAGGAAAGATAGAAATGAAGGCAATTAAGAATGAACCTCACAAGAGAAATTTATACA 1053
QY 895 ACTGAATTAATTTTGAACCGCTTACTTACTCTTGAATTAACCCCAATCTCGCTATAATG 954
DB 1054 ACTGAATTAATTTTGTATCGTCTTCTCACTTAGAGTTCAACCCCAATCTAGTACGATG 1113
QY 955 GAATATAATTTAACACGTTTCAGGGCTTAGATATATTTTCAATTTTATAGATGAACCTTATTT 1014
DB 1114 GAATATAATTTAACACGTTTCAGGGCTTAGATATATTTTCAATTTTATAGATGAACCTTATTT 1173
QY 1015 TATACAAAAATGAACGTTACGGGAATCGTTAGTTGGTATTCGGAATCGTAAATAGATCT 1074
DB 1174 TATACAGAAAAATACAAATTTTCGGGAATCGTTAGTTGGTATTTCTAATCGTATGACCT 1233
QY 1075 ACTTATGCTACGACGGAATGAAATATATATATGGAAGAACAGACGTCACCCCAACA 1134
DB 1234 ACTTATAGCAATACTATACTGAACTTTATATGGAAGAACAGACGTCACCCCAACA 1293
QY 1135 AAAACTTTTATACCATTTGAATCCTATAAAGTTTCAATTTGTAACCTGATAGCAAGTAACT 1194
DB 1294 AAAACAAATAGACCATTTGAACTTTTAAAGTTTCAATTTGTAACCTGATAGCAACATCACCT 1353
QY 1195 CCTACTTCCCTTTTCTAACATATATCTTTCAATTAATCAAAATTTGAACCTTATTTAAAT 1254
DB 1354 CCTGTTTCCCTTATTC---AACCACTTTTATAATTAATCAAAATTTGAACCTTATTTAAAT 1410
QY 1255 AATTCACCTAGTAAATTAATTAACATATTCAGCTGGGGGAATTTATCTAATGATATAAAAA 1314
DB 1411 GGCTCATCTTAACACACACTCAAAATATTCAGCAGGAGGGTCTTTATCTAATTTCAAAAC 1470
QY 1315 ACAACTGATTTTCAATTTCTGTAAAAAAGACAGCTGTAACCAATTTAATTTCAAAATGTT 1374
DB 1471 ACAACTTTTTCATTTCTCTAGAAAAAAGACAGCTGCAATCTAGTTATTTGATCCAGGTTGT 1530
QY 1375 TTACCAAGCTTATTAATAGTTATAGTCATATTTTATCCAGTTTCTTTTATTTTAAATTTTCC 1434
DB 1531 TCACCAAACTTTAATTAATCTATAGTCATATTTTATCCCATTTTTCATTTATTTTACTTTTCC 1590
QY 1435 TATAAAAATTCGATTTAGCGCTAAATATATATATATATACAGGTGCTAGGATGGACACAGT 1494
DB 1591 TATGTGATTTGGATTTACAGCTACAAATATTTAGATACAGGTGATTTAGGATGGACACAGT 1650
QY 1495 AGTGTTAATAAGAAATTAATGCAATATCAGATAAAATTAATTAACAATGATCCAGCAATCAA 1554
DB 1651 AGTGTGATAGATATATGCAATATCAGATAAAATTAATTAACAATGATCCAGCAATCAA 1710
QY 1555 GGTAACAGCTCTTGATACAAACTCTAAGGTAATTTGAAGGACCTGTGTCATACAGGAGGAAC 1614
DB 1711 GGTAACAACTCTTGATACAAACTCTAAGGTAATTTGAAGGACCTGTGTCATACAGGAGGAAC 1770
QY 1615 TTGGTTTATTTACAAAGCTCAAGGGCTTTAGAGATTTACATGTAGAACTCCCTAAATTTCTACA 1674
DB 1771 TTGGTTTATTTACAAAGCTCAAGGGCTTTAGAGATTTACATGTAGAACTCCCTAAATTTCTACA 1830
QY 1675 CAATCTTATTTACATTTAGACTTTTCGATACCAATGCTGCGAAATFACCTTCTTCTTAAT 1734
DB 1831 CAATCTTATTTTCAATTTAGACTTTTCGATACCAATGCTGCGAAATFACCTTCTTCTTAAT 1890
QY 1735 ATATCTCTTCAATATACAGGAGTAAATAGGAATAACAACCTCAACGACTCAACACACTTTT 1794

1991	ATATCTCTTACAAATACACGAGNGTAATAGGAATATACCACTCAACGACTCAACAACACTTTT	1950
1795	TCTGGTACAAATTATAATAATTTTACAATACGGAGATTTTGGGTATTTTCCAAATTTCCAAAGT	1854
1951	TCTGGTACAAATTATAATAATTTTACAATACGGAGATTTTGGGTATTTTCCAAATTTCCAAAGT	2010
1855	ACAGTACATTTACCTTTTAAATTCGAAACATACCACTTATTTAATCTCGTGCAGATGTATCA	1914
2011	ACAGTACATTTACCTTTTAAATTCGAAACATACCACTTATTTAATCTCGTGCAGATGTATCA	2070
1915	AATTCAAATTTTAAATCATTTGATATAAAATTTGAATTTTATACCAATTTACTTCTCTGTACGCCAA	1974
2071	AATTCAAATTTTAAATCATTTGATATAAAATTTGAATTTTATACCAATTTACTTCTCTGTACGCCAA	2130
1975	AATAGAGAAAACAAAATTTAGAACTTATCCAAACAAAATAAATACATTTTTTTCACAAAT	2034
2131	AATAGAGAAAACAAAATTTAGAACTTATCCAAACAAAATAAATACATTTTTTTCACAAAT	2190
2035	CATACAAAAAATACTTTTA	2052
2191	CATACAAAAACACTTTTGA	2208

RESULT 4

RESOL 4
AAN93054
ID AAN93054 standard: DNA: 3940 BP.

XX	AAAN93054 standard; DNA, 3510 bp.
XX	
XX	AAAN93054;
XX	
DT	27-AUG-2003 (revised)
DT	25-MAR-2003 (revised)
DT	30-MAY-1990 (first entry)

XX	Delta-endotoxin crystal protein gene.
DE	
XX	Delta-endotoxin; crystal protein; insect biological control agent.
KW	
KW	
XX	<i>Bacillus thuringiensis israelensis</i> .
OS	

XX	Key	Location/Qualifiers
PH	RBS	879. .884
FT		/*tag= b
FT		/label= Shine-Delgarn
FT	CDS	891
FT		/*tag= a
FT		/product= "delta-end
XX		
PN	EP296870-A.	
XX		
PD	28-DEC-1988.	
XX		
PF	24-JUN-1988;	88EP-00305772.
XX		
PR	26-JUN-1987;	87US-00067653

XX
PA
XX
PI
XX
DR
DR
XX

(DUPO) DU PONT DE NEMOURS & CO E I.

Ellar DJ, Ward ES;

WPI; 1989-001322/01.
P-PSDB; AAP94035.

XX
PT
PT
PT
PT

DNA fragment encoding insecticidal protein - obtd. from *Bacillus thuringiensis* sub species israelensis, and used in microorganisms and plant Cells.

XX	SQ	Sequence	3940 BP; 1457 A; 603 C; 659 G; 1221 T; 0 U; 0 Other;
		Query Match	16.0%; Score 334.6; DB 1; Length 3940;
		Best Local Similarity	53.9%; Pred. No. 1.1e-46;
		Matches	858; Conservative 0; Mismatches 695; Indels 38; Gaps 7;
Qy	499	TATAAAACGCTATTACTACCTATTATTATGCGCAAGCTGCTAAATTTTCATTTAAATTTATTATTA	558
Db	1494	TATAACATATAGTATTATCTAGTATTGACACAGCAGCAAACTTACATCTGACTGTATTATTA	1553
Qy	559	CAACAAGGTGCTCAATTTGGCTGATGAATGGAATGCAAGTATATACCTCTTCACAAAATTGAA	618
Db	1554	AATCAAGCCGTCAAATTTGAAGGTTATTTAAAAACAATCGACAATTCGATTATTTTAGAG	1613
Qy	619	CCTAATGCTGGAAATCATCAGATGACTATTATAAAGCTTTTAAAGAGAAATATACCTAAATAT	678
Db	1614	CCTTTGCC---AACAGCAATTTGATTATTATCCAGTATTGACTAAAGCTATAGAAGATTAC	1670
Qy	679	AGTAACCTATTGTGCAAAATCCTATACAGAGGAGCTAAATAAACTTCGAAACGAACCTAAT	738
Db	1671	ACTAATATTGTGTAACTATTATAAAGAGTTAAATTTAATTTAAACGACGCTGAT	1730
Qy	739	ATCAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTTAGATACT	798
Db	1731	AGTAATCTTGATGGAATATATAACTGGAACACATACATACGTATCGAAACAAAATGACT	1790
Qy	799	ATCGCTCAATTTCTTTTATGATATATAGAGATACAGAGATTCATATAGNAGAAATAGGT	858
Db	1791	ACTGCTGTATTAGATGTGTGCACTCTTTCCCTAAATTATGATGTAGGTAAATATCCAAATA	1850
Qy	859	GGCAATTAACAACTGAACTTACAGAGAAATTTATACAACTGAAATAAAATTTTGACCGCTCTT	918
Db	1851	GGTGTCCNATCTGAACTTACTCGAGAAATTTAT-----CAGGTACTTTAACTTCGAAGA	1903
Qy	919	ACTTACCTTGAATTCAAACCCAACTCTCGCTATTAATGGAATATATTTTAACAGCTTCAGGG	978
Db	1904	AAGCCCTATAAATATATTAGACTTCCAATATCAAGAGGATTCACTTTACAGCTAGACCGCA	1963
Qy	979	CTTAGATATATTTTCATTTTATAGATGAACCTTATATTTTATACAAAAATGAAACGTACGGG	1038
Db	1964	TTTATTACTCTGGCTTGATCTTTTGAATTTTATGAAAAGCGCAAACTACTCTTAATAA	2023
Qy	1039	AATCGTTTAGTTAGTTATGCGAATCGTAATAGATCTACTTT-ATGCTACGACAGGAAGTGA	1097
Db	2024	TTTTTTTACCAGCCATTATAATATGTTTCAATTACACACTTGATAATATATCCCAAAATC	2083
Qy	1098	AATATATATGGAGAAGAACAGGTCACCCCAACACAAAACTTTAATAACCATTTTGAATC	1157
Db	2084	TAGTGTTTTGGAAATCACAATGTAACCTGATAAATTTAAATCTCTTGGTTTGGCAACAA	2143
Qy	1158	CTATAAAGTTTCAATTTGTAACCTGATAGCAAGTAACCTCTACTTCCCTCTTTTCTTAACAT	1217
Db	2144	TATTTATATTTTTTATTTAAATGTCATAAGCTTAGATAATATAATATCTAAATGATTATAA	2203
Qy	1218	ATACTTTACAAATTAATCAAAATGGAACCTTTATTTAAATAATTTACCTAGTAAATAAATTAAC	1277
Db	2204	TAATATATTAGTAAATTCGATTTTTTTTATAACTAATGGTACTAGACTTTTGGAGAAAGAACT	2263
Qy	1278	ATATTACAGCTGGGGGAAATTTATCTAATGATAAAAAACAACCTGATTTTTCATTTTCTCTGT	1337
Db	2264	TACAGCAGGATCTGGGCAATAACTTATGATGTAAATAAATAATTTTTCGGGTACCAAT	2323
Qy	1338	AAAAAAGACTGPAACCAAAATTTAATCAAATGTGTTTACCAAGCTATAATAGTTATTAG	1397
Db	2324	TCTTAAACGAGAGAGAAATCAAGGAAACCGCTACCCCTTTTTCCAACATATGATAACTATAG	2383
Qy	1398	TCATATTTTATCCAGTTTTCTTTATTTAATTTATTCCTATAAATTTGGATTAGCGCTAAA	1457
Db	2384	TCATATTTTATCATTTTATTAAGTCTTAGTATCCC-----TGCAACATA	2428
Qy	1458	TATATTTATATACAGGTGCTATTAGGATGGACACACAGTAGTGTTAATAGAAATAATGCAAT	1517

Db	2429	TAAACTCAAGTGATACAGTGGTTGCTTGGACACACTAGTGGTTGATCTCAATAAATAACAAT	2488
Qy	1518	ATCAGATAAATAATTAACAATGATCCAGCAATCAAGGTAAAGTCTTGATCAAACTC	1577
Db	2489	TTATACACATTTAACTACCCAAATTCAGCTGTAAAAGCGAATTCACCTTGGGACGCTTC	2548
Qy	1578	TAAGGTAAATTAAGGACCTGGTCATACAGGAGGAACTTGGTTATTACAAAGTCAAGG	1637
Db	2549	TAAGGTGTTCAAGGACCTGGTCATACAGGAGGAACTTAAATGATTTCAAGATCA---	2605
Qy	1638	GCCTTTAGAGATTACATGTAGAACTCCTAATCTACACAATCTTATACATTTAGACTTGG	1697
Db	2606	---TTTCBAATTTACATGTCAACACTCAAAATTTTCAACAATCGTATTATTATAAGAAATCG	2662
Qy	1698	ATACGCTACAAATGGTCTGGAAATCTCTTCTTAATATATATCTTCTCAATATACAGAGT	1757
Db	2663	TTATGCTTCAAAATGGAAGCGCAAAATCTCGAGCTGTTTATAAATCTTAGTATCCAGGGT	2722
Qy	1758	AATAGGAATACCCTCAACGACTCAACAACACTTTTCTGTACAAATTTATATAATTT	1817
Db	2723	AGCAGAACTG---GGTATGGCACTCAACCCCACTTTTCTGGTACAGATTATACGAATTT	2779
Qy	1818	ACAACTCGAGATTTTGGGTATTTCCAAATTTCCAAATGACAGTAACTTAAATCG	1877
Db	2780	AAATATAAAGATTTTCAGTACTTAGAATTTTCTAACGAGTGAAATTTGCTCCAAATCA	2839
Qy	1878	AAACATACCAATTTATATTTAATCGTGAGATGAT---CAAATTCAAATTTTAAATCATGA	1934
Db	2840	AAACATATCTCTTGTTTAAATCGTTCGGATGTATATACAAACACACAGTACTTATTGA	2899
Qy	1935	TAAATTTGAATTTATACCAATTTACTCTCTGTACGCGCAAAATAGAGAAAACAAAAAT	1994
Db	2900	TAAATTTGAATTTCTGCAATTTACTCGTTCTAAGAGAGATAGAGAAACAAAATTT	2959
Qy	1995	AGAACTATCAAAACAAAATAAATACATTTTTCACAAATCATACAAAAATCTTTAA	2054
Db	2960	AGAACTAGTACAAATATTAATATACATTTTATGCHAAATCTTATAAAACACTTTTACA	3019
Qy	2055	TATAGAGCCCAAACTATGATTTGATTAA	2085
Db	3020	ATCAGAACTTACAGATTATGACATAGATCAA	3050
Db	AAAN93059 standard; DNA; 4571 BP.		
AC	AAAN93059;		
XX	27-AUG-2003 (revised)		
DT	25-MAR-2003 (revised)		
DT	30-MAY-1990 (first entry)		
XX	Delta-endotoxin crystal protein gene.		
DE	Delta-endotoxin; crystal protein; insecticide; pch130; ss;		
KW	biological control agent.		
XX	Bacillus thuringiensis; israelensis.		
XX	Location/Qualifiers		
FH	879. .884		
RBS	/*tag= b		
FT	/label= Shine-Dalgarno sequence.		
FT	891. .4430		
FT	/*tag= a		
FT	/product= "delta-endotoxin crystal protein"		
XX	EP296870-A.		
PN	28-DEC-1988.		
PD	24-JUN-1988; 88EP-00305772.		
XX			
PF			

XX	26-JUN-1987; 87US-00067653.
PR	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	
PA	Ellar DJ, Ward ES;
XX	
PI	WPI; 1989-001322/01.
XX	P-PSDB; AAP93715.
DR	
DR	DNA fragment encoding insecticidal protein - obtd. from Bacillus
XX	thuringiensis sub species israelensis, and used in microorganisms and
PT	plant cells.
PT	
XX	Disclosure; Fig 7; 26pp; English.
PS	
XX	The sequence encodes the 130 kDa delta-endotoxin gene from B.
CC	thuringiensis subsp. israelensis and is a 4.46 kb insert of pch130. The
CC	delta endotoxin protein is insecticidal and can be used to control insect
CC	pests esp. mosquitos. See also AAN93054. (Updated on 25-MAR-2003 to
CC	correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
XX	
SQ	Sequence 4571 BP; 1678 A; 685 C; 817 G; 1391 T; 0 U; 0 Other;

Query Match	16.0%;	Score 334.6;	DB 1;	Length 4571;
Best Local Similarity	53.9%;	Pred. No. 1.1e-46;		
Matches	859;	Conservative 0;	Mismatches 695;	Indels 38; Gaps 7;

Qy	499	TATAAACGGTATTACTACCTATTATGCGCAAGCTGCTAAATTTTCATTTTAAATTTATTA	558
Db	1494	TATAACATACTAGTATTATCTAGTTATGCAACAGCAGCAAACTTACATCTGACTGTATTA	1553
Qy	559	CAACAAGGTCCTCAATTTGGCTGATGAATGGAATGCAGATATACATCTTCCACAAATTTGAA	618
Db	1554	AATCAAGCGCTCAATTTGAAGCGTATTAAACAAACATCGACAATTCGATTATTTAGAG	1613
Qy	619	CCTAATGCTGGACATCAGATGACTATTATAAACTTTTAAAGAAAATATACCTAAATAT	678
Db	1614	CCITTTGCC---NACAGCAATTTGATTATTCAGTATTTGACTAAAGCTATAGAAGATTAC	1670
Qy	679	AGTAACTATTGTGCAAAATACCTATAGAGAGAGGACTAAATAAACTTCGAAACGAACTTAT	738
Db	1671	ACTAATTTATTGTGTAAACAACCTTATAAAAGAGATTAATAATTTAAATAAGACGCCCTGAT	1730
Qy	739	ATGAGATGGAGTATTATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT	798
Db	1731	AGTAATCTTGATGGAATATAAATACTGGAACACATACATAGCTATCGAACAAATAGCT	1790
Qy	799	ATCGCTCAATTTTCTTTTATGATATAAGAGATACAAAGATTCATAGGAAGATAGGT	858
Db	1791	ACTGCTGATTAGATGTTGTTGCACTCTTTCTTAATTTATGATGATGAGTAAATATCCAATA	1850
Qy	859	GGCAATTAATACTGAACTTACAGAGAAATTTATACAACTGAAATAAATTTTTCAGCGTCTT	918
Db	1851	GGTGTCCAATCTGAACTTACTCGAGAAATTTAT-----CAGGTACTTAACCTTCGAAGA	1903
Qy	919	ACTTACCTTGAATTTCAACCAATCTCGCTATATGGAATATAATTTAAACAGCTTCAGGG	978
Db	1904	AAGCCCTATAAATATTATGACTTTCAATATCAAGAGATTCATTCACGCTAGACCGCA	1963
Qy	979	CTTAGATTATTTTTCATTTTATAGATGAACCTTATATTATTAACAAAATAAGAACTGACGGG	1038
Db	1964	TTTATTTACTTGGCTTCTGATTTCTTTGAAATTTTATGAAAAGGCGCAAACTACTCTCTAA	2023
Qy	1039	AATCGTTTAGTGTGATTTGGAATCGTAATAGATCTACTTT-ATGCTAGCAGGAGACTGA	1097
Db	2024	TTTTTTCACCAGCCATTAATATATGTTTTCATTCACACTTGTATAATATATCCCAAAATC	2083
Qy	1098	AATTATATATGAGAGAAAGACAGGTCCACCACCAACAAAATACTTTTAAATCATTTGATC	1157
Db	2084	TAGTGTTTTGGAAATCACAATGTAATGTAATTAATCTCTTGGTTTGGCAACAA	2143
Qy	1158	CTATAAAGTTTCAATTTGTAACACTGATAGACAAGTAACTCCTACTTCCCTCTTCTTAACAT	1217

Db 2144 TATTTATATTTTTTAAATGTCATAAGCTTAGATAATAAATATATCTAAATGATTATAA 2203
Qy 1218 ATACTTTACAAATTAATCAAAATCGAATCTTTATTTAAATAAATTCACCTAGTAGTAATAAATAAC 1277
Db 2204 TAATATTTAGTAAATGGAATTTTTTATTAACATAATGGTACTAGACTTTTGGAGAAAGAACT 2263
Qy 1278 ATATTGAGCTGGGGGAAATTTATCTAATGATAAATAAACAACCTGATTTTCAATTTCTCTGT 1337
Db 2264 TACAGCAGGATCTGGGCAATAACTTTATGATGATAATAAATAAATTTTCGGGTACCAAT 2323
Qy 1338 AAAAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCAGCTATAATATTATTAG 1397
Db 2324 TCTTAAACGAGAGAGAAATCAAGGAACCCCTACCTTTTCCAAATATGATGATAACTATAG 2383
Qy 1398 TCATATTTTATCCAGTTTCTTTTATTTAATTAATTCCTATAAAAAATTCGATTAGCGCTAAA 1457
Db 2384 TCATATTTTATCATTTATTAAGAGCTTAGTATCCC-----TGCACATA 2428
Qy 1458 TATATTATATACAGGTGCATTAGATGGACACACAGTAGTGTTAATAGAAAAATTAATGCAAT 1517
Db 2429 TAAAACTCAAGTGATACGTTTGTCTGGACACACTCTAGTGTTCATCTTAAAAATACAAT 2488
Qy 1518 ATCAGATAAATAATTAACATATGATCCAGCAATCAAGGTAAACAGCTCTTGATACAACTC 1577
Db 2489 TTATACACATTTAACTACCCAAATTCAGCTGTAAAAGCGAATTCACCTGGGACTGCTTC 2548
Qy 1578 TAAGGTAAATTAAGAGGACTCGTGCATACAGAGGAAACTTGGTTTATTTACAAAGTCAAGG 1637
Db 2549 TAAGGTGTTCAAGGACCTGGTGCATACAGAGGGGATTTAATTTGATTTCAAGATCA--- 2605
Qy 1638 GCCTTTAGATTCATATGATAGAACTCTTAATTTTACACAACTTATTAATAGACTTCG 1697
Db 2606 ---TTTCAAAATTTACATGTCAACACTCAAAATTTTCAACAACTCGTATTTTATAAGAAATCG 2662
Qy 1698 ATAGCTACAAATGGTGCTGGAATATCTCTCTAATATATCTTTACAAATACCGAGT 1757
Db 2663 TTATGCTTCAAAATGGGAAGCGCAATTAATCGAGCTGTATTAATCTTTAGTATCCAGGGT 2722
Qy 1758 AATAGGAATACCACCTCAACGACTCAACAACTTTTCTGGTACAAATTAATAATTT 1817
Db 2723 AGCAGAACTG---GGTATGCACTCAACCCACTTTTCTGGTACAGATTTATACGAATTT 2779
Qy 1818 ACAATACGGAGATTTTGGGTATTTCCAAATTTCCAAGTACAGTAACTTACCTTTTAAATCG 1877
Db 2780 AAAATATAAAGATTTTCAGTACTTAGAATTTTCTAACGAGGTGAATTTGCTCCAAATCA 2839
Qy 1878 AAACATACCAATTTATATTTAATCGTCAGATGTAT---CAAAATTCAAATTTTATCATTTGA 1934
Db 2840 AAACATATCTCTGTGTATTAATCGTTGGATGTATATACAAACACACAGTACTTTATTGA 2899
Qy 1935 TAAAAATGAATTTATACCAATTTACTTCTCTGACGCCAAATATAGAGAAAAACAAAAAT 1994
Db 2900 TAAATTTGAATTTCTGCCAATTTACTCGTTCTATAGAGAGGATAGAGAGAAACAAAAAT 2959
Qy 1995 AGAACTATCCAAACAAAAATAAATACATTTTTCACAAATFCATACAAAAATACCTTTAA 2054
Db 2960 AGAAACAGTACAAACAAATAATTAATACATTTTATGCAATCTCTATAAAAAACCTTTACA 3019
Qy 2055 TATAGAGCCACAACATCATGATTTGATTAA 2085
Db 3020 ATCAGAACTTTACAGATTTATGACATAGATCAA 3050

RESULT 6
AA81490
ID AA81490 standard; DNA; 4934 BP.
XX
AC
XX AA81490;
XX
DT 24-OCT-2003 (revised)
DT 05-NOV-1990 (first entry)
XX

Insecticidal (Diptera) protein gene.
XX
KW Insecticidal protein gene; Diptera; Aedes; ss.
XX
OS Bacillus thuringiensis serovar israelensis.
XX
FH Key Location/Qualifiers
CDS 1..4908
FT /*tag= a
FT /product= "insecticidal protein"
FT 620..1368
FT /tag= b
XX
PN JP63230090-A.
XX
PD 26-SEP-1988.
XX
XX 19-MAR-1987; 87JP-00066844.
XX
PR 19-MAR-1987; 87JP-00066844.
XX
XX (SUMO) SUMITOMO CHEM IND KK.
PA WPI: 1988-311968/44.
DR P-PSDB; AAP81034, AAP82589.
XX
XX New insecticidal protein of bacillus tulingensis islaerensis strain -
PT prepd. by isolating plasmid contg. insecticidal protein gene by forming
PT gene library from plasmid deoxyribonucleic acid, etc.
XX
PS Disclosure; Page ?; 9pp; Japanese.
XX
CC A plasmid contg. the gene is isolated by forming a gene library from
CC plasmid DNA of B.thuringiensis israelensis (HD 522 strain, USA Goldberg
CC CNR60) followed by screening with anti-israelensis insecticidal protein
CC IG. The insecticidal protein is highly effective against Diptera, esp.
CC Aedes. (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 4934 BP; 1797 A; 749 C; 877 G; 1511 T; 0 U; 0 Other;
Query Match 16.0%; Score 334.6; DB 1; Length 4934;
Best Local Similarity 53.9%; Pred. No. 1.1e-46;
Matches 858; Conservative 0; Mismatches 695; Indels 38; Gaps 7;
Qy 499 TATAAAACGCTATTACTACTATTATGCGAAGCTGCTAAATTTTCATTTAAATTTATTA 558
Db 1972 TATAACATATAGTATTATCTAGTTATGCACAAGCAGCAAACTTACATCTGACTGTATTA 2031
Qy 559 CAACAGGTGCTGAATTTGGCTGATGAATCGAATGCAGATATACATCTTCACAAATTTGAA 618
Db 2032 AATCAAGCCGTCAAAATTTGAAGCGTATTTAAAAAACAATCGACAATTCGATTATTAGAG 2091
Qy 619 CCTAATGCTGGAACATCAGATGACTATTATAAACTTTTAAAAAGAAATATACCTAAATAT 678
Db 2092 CTTTGGC---ACAGCAATTTGATTATTATCCAGTATGACTAAAGCTATAGAAGATTAC 2148
Qy 679 AGTAACATATGTGCAAAATACCTATAGAGAAAGCTAAATAAAGCTTCGAAACGAACTTAAT 738
Db 2149 ACTAATTTATGTGTAACTTATAAAAAAGGATTTAAATTTAAATTTAAAAACGACGCTGAT 2208
Qy 739 ATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT 798
Db 2209 AGTAATCTTTGATGGAAATATAAACTGGAAACACATACATACGTATCGAACAAAAATGACT 2268
Qy 799 ATCGCTCAATTTTCTTTTATGATATAAGAGATACAAAGATTTCATATAGAGAAATAGGT 858
Db 2269 ACTGTGTTATAGATCTTGTGCACTCTTTCTCTAATATGATGTAGTAAATATCCAATA 2328
Qy 859 GGCATTTAAACCTGAACCTTACAGAGAAATTTATACAACTGAAATAAATTTTGGACGCTTT 918
Db 2329 GGTGTCCAATCTGAACCTTACTCGAGAAATTTAT-----CAGGTACTTAACTTCGAAGA 2381
Qy 919 ACTTACCTTGAATTTCAACCCCAATCTCGCTATAATGGAATATAATTTTAACACGCTTCAGG 978

Db	2382	AGGCCCTATAAATATATGACCTTTCATATATCAAGAGGATTCACCTACACGTAGACCGCA	2441
Qy	979	CTTAGATTATTTTCATTTTATAGATGAACCTATATTTTATACAAAAATGAAGCGTAGCGGG	1038
Db	2442	TTTATTTACTTGGCTTGATTTCTTTGAATTTTATGAAAAAGCGCAACTACTCTTAATAA	2501
Qy	1039	AATCGTTTATGTTGGTATTCGGAAATCGTAATAGATCTACTTT-ATGCTACACAGGAACTGA	1097
Db	2502	TTTTTTTCCACGACCATATATAATATGTTTCATTACACACTTGATATATATATCCAAAAATC	2561
Qy	1098	AATTATATATGAGAAAGACAGGTCACCCACACAAAAAATTTTAAATACCATTTTGAATC	1157
Db	2562	TAGTGTGTTTGGAAATACAAATGTAATCTGATTAATTTAAATCTCTTGGTTTGGCAACAA	2621
Qy	1158	CTATAAAGTTTCAATTTGTAACCTGATAGACAAGTAACCTCTACTTCCCTTTTCCCTAACT	1217
Db	2622	TATTTATATTTTATTAATGTCATAGCTTAGATAATAATATCTAAATGATTATAA	2681
Qy	1218	ATACTTTACAATTAACAAATGAACTTTTATTTAAATTAATTCACCTAGTAATAAATTAAC	1277
Db	2682	TAATATTAGTAAATGGAATTTTATTAACCTAATGCTACTAGACTTTTGGAGAAAGAACT	2741
Qy	1278	ATATTGAGCTGGGGGAATTTATCTAATGATTAATAAAAAACAACCTGATTTTCAATTTCTCTGT	1337
Db	2742	TACAGCAGGATCTGGGCAATAACTTATGATGTAATAAATAAATATTTTCGGGTACCAAT	2801
Qy	1338	AAAAAAGACTGTAAACCAATTAATTAATCCAAATGTTTACCAAGCTATAATATGTTATAG	1397
Db	2802	TCCTAAACGAGAGAGATCAAGAAACCTACCTTTTCCAAATATGATAACTATAG	2861
Qy	1398	TCAATTTTATCCAGCTTTCTTTTATTAATTAATCTCTATAAATTTGGATTAGCGCTAA	1457
Db	2862	TCATATTTTATCTTATTAATAAAGTCTTAGTATCCC-----TGCAACATA	2906
Qy	1458	TATATTATATACAGGTGCATTAGATGACACACAGTAGTGTTAATAGAAATATGCAAT	1517
Db	2907	TAAAACTCAAGTGATACGTTTCTGTTGGACACACTCTAGTGTTGATCTCTAAATAATCAAT	2966
Qy	1518	ATCAGATAAATAATTAACAATGATCCAGCAATCAAGGTAACAGCTCTTGATACAAATC	1577
Db	2967	TTATACATTTAACTACCAATTCAGCTGTAAAGCGAATTCACCTGGGAGTGGTTC	3026
Qy	1578	TAAAGGTAATTTGAAGGACCTGGTCATACAGGAGAACTTGGTTATTTAACAAGTCAAGG	1637
Db	3027	TAGGTTGTTCAAGGACCTGGTCATACAGGAGGGATTTAAATGATTTCAAGATCA---	3083
Qy	1638	CGGTTTAGAGATTACATGTAGAACTCTTAATCTACACAATCTTATTACATTAGACTTCG	1697
Db	3084	---TTTCAAAAATTACATGTCAACACTCAAAATTTTTCACATCGTATTTTATAGAAATCG	3140
Qy	1698	ATAGCTACAAATGGTGTGGAATATCTTCTTAAATATCTCTTACAAATACAGAGAT	1757
Db	3141	TTATGCTTCAAAATGGAAGCGCAATCTCGAGCTGTTTAAATCTTAGTATCCAGGGGT	3200
Qy	1758	AATAGGAATACCACTCAACGACTCAACACACTTTTCTGGTACAAATTAATAAATTT	1817
Db	3201	AGCAGACTG---GGTATGGCACTCAACCCACATTTTCTGGTACAGATTATACGAATTT	3257
Qy	1818	ACAAATCGGAGATTTGGGTATTTTCCAAATTTCCAAATGATACAGTACATCTTTAAATCG	1877
Db	3258	AAAATATAAGATTTTCAGTACTTAGAATTTTCTTAACGAGGTGAAATTTGCTCCAAATCA	3317
Qy	1878	AAACATACATTTATATTTATCTGGCAGATGAT---CAAATTTCAATTTTAAATCATGTA	1934
Db	3318	AAACATATCTCTTGTGTTTAAATCGTTCGGATGATATACAAACACACAGTACTTTTGA	3377
Qy	1935	TAAATTTGAAATTTATACCAATTTACTTCTCTGTAGCCAAATATAGAAAAACAAAAAT	1994
Db	3378	TAAATTTGAAATTTCTGCCAATTTACTCTGTTCTATAGAGAGGATAGAGAGAAACAAAAAT	3437
Qy	1995	AGAACTATCCAAACAAAAATAAATAATATATTTTTCACAAATCATACAAAAATCTTTAA	2054

3438 AGAAACAGTACAAACAAATAAATTAATACATTTTATGCAAAATCTTATAAAAAACACTTTTACA 3497

2055 TATAGAACCCACAACTATGATATTGATTAA 2085

3498 ATCAGAACTTACAGATTATGACATAGATCAA 3528

RESULT 7

AAQ14669

ID AAQ14669 standard; DNA; 3543 BP.

XX AAQ14669;

AC

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 04-FEB-1992 (first entry)

XX Dipteran active toxin gene.

XX Insecticide; B.t; crystal; delta endotoxin; cryIIA; ss.

XX Bacillus thuringiensis serovar morrisoni.

OS

FH Key Location/Qualifiers

FT 1. .3543

FT CDS /*tag= a

XX EP457498-A.

XX 21-NOV-1991. 91EP-00304180.

XX 09-MAY-1991; 91EP-00304180.

XX 15-MAY-1990; 90US-00524255.

PR 01-OCT-1990; 90US-00590903.

XX (MYCO) MYCOGEN CORP.

XX Sick AJ;

XX WPI; 1991-341902/47.

DR P-PSDB; AARI4373.

XX Bacillus thuringiensis genes encoding diptera-active toxins - and transformed microbes used to control insects in various environments.

PS Claim 1; Page 10; 20pp; English.

XX The sequence was obtd. from plasmid pMYC1625 which was isolated from a genomic library prepd. from DNA from B.t. PS71M3 [from B.t. PS71M3-69 (NRRL B-18515)]. It is related to the cryIIA family of genes, the 140 kD endotoxin gene and the type II gene from B.t. var. israelensis. The gene encodes a 130 kD protein. Microorganisms transformed with the DNA may be administered to dipteran insects or their environments, the expressed toxins acting as an insecticide. See also AAQ14670-Q14672. (Updated on 25 -MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 3543 BP; 1278 A; 567 C; 612 G; 1086 T; 0 U; 0 Other;

Qy Query Match 15.9%; Score 331.4; DB 2; Length 3543;

Db Best Local Similarity 53.8%; Pred. No. 3.7e-46;

Qy Matches 856; Conservative 0; Mismatches 697; Indels 38; Gaps 7;

Qy 499 TATAAAAACGCTATTACTACCTATTATGCGCAAGCTGCTTAATTTTCAATTTTAAATTTTATA 558

Db 604 TATAACATACATAGTATTATCTAGTTATGCAACAGCAGCAAACTTACATCTGACTGTATTA 663

Qy 559 CAACAAGGTGCTGAATTTGGCTGATGGAATGCAATGCATATACATCTTCCAAATTTGAA 618

Db 664 AATCAAGCCGCTCAAAATTTGAAGCGGTATTTAAAAAACAATCGACATTCGATTATTAGAG 723

Qy 619 CCTAATGCTGGAACATCAGATGACTATTATAAACTTTTAAAAAGAAAAATATACCTAAATAT 678

Db 724 CTTTCC---AACAGCAATTGATTAATCCAGTATTCAGTAAAGCTATAGAAATTAC 780
QY 679 AGTAACATTGTGCAAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACTAAT 738
Db 781 ACTAAATTATGTGTAACAACCTTATAAAAAGGATTAAATTTAATTAAACGACGCTGAT 840
QY 739 ATGAGATGAGATATATTAATGATTATCGAAGATATATGACTATTAATGATTAGATAT 798
Db 841 AGTAATCTTTGATGAGAAATAAACTCGAACAACATACGATATCGAACAATAATGACT 900
QY 799 ATCGCTCAATTTCTTTTATGATATAAAGAGATACAAGAGATTCAATAGGAAGAAATGAGT 858
Db 901 ACTGCTGATATAGATCTGTGCACTCTTTCCTAATTATGATGATAGTAAATATCCATA 960
QY 859 GGCATTAAACCTGAACCTTACAAGAGAAATTTATPACAACTGAAATAAAATTTTGACCGTCT 918
Db 961 GGTGTCCAATCTGAACCTTACTCGAGAAATTTAT-----CAGGTACTTTAACTTCGAAGA 1013
QY 919 ACTTACCTTGAATTCGAACCAATCTCGCTATATGCGAATATATTTAAACACGTTCCAGG 978
Db 1014 AAGCCCTTATAATATATGACTTTCAATATCAAGAGGATTCACTTACACGCTAGACCGCA 1073
QY 979 CTTAGATTATTTCTTTTATGATGAACCTTATATTTTACAAAAATGAAAGCTACGGG 1038
Db 1074 TTTATTTACTTGGCTTGATCTTTTGAATTTTATGAAAAAGCGCAAACTACTCTCTAATAA 1133
QY 1039 AATCGTTTATGTTGTTATCGAATCGTAAATAGATCTACTT-ATGCTACGACAGGAACTGA 1097
Db 1134 TTTTTTACCAGCCATTATAATATGTTTCATTACACACTTGATATATATATCCAAAAATC 1193
QY 1098 AATTATATATGAGAAAGAACAGTCCACCCACACAAAACTTTTAATACCATTTGAATC 1157
Db 1194 TAGTGTTTTGGAAATCACAATGTAACTGATATAAATTTAAATCTCTTGGTTTGGCAACAA 1253
QY 1158 CTATAAGTTTCAATTTGTAAGTATAGACAAGTAACCTCTACTTCCCTTTTCTTAAACAT 1217
Db 1254 TATTTATATTTTTTATTAATGTCTAAGCTTAGATATAATATCTAAATGATTATAA 1313
QY 1218 ATACTTTACAATTAATCAAAATGAACTTTATTTAAATAATTCACCTAGTAATAAATTAAC 1277
Db 1314 TAATATTAGTAAATGGAATTTTTTATAACTAATGGTACTAGACTTTTGGAGAAAGAACT 1373
QY 1278 ATATTCAGCTGGGGGAAATTTATCTAATGATATAAAAAACACTGATTTTCAATTTCTCTGT 1337
Db 1374 TACAGCAGGATCTGGGCAAAATAACTTATGATGTAAATAAAAAATATTTTCGGTTTACCAAT 1433
QY 1338 AAAAAAGACTGTAAACCAATTTATTAATCCAAATGTTTTACCAAGCTATAATAGTTATAG 1397
Db 1434 TCTTAAACCAAGAGAAATCAAGCAATCCCTACCTTTTCCACATATGATTAATAG 1493
QY 1398 TCATATTTTATCCAGTTTTCTTTATTTTAAATTTATTCCTATAAAATTTGGATTAGCGCTAA 1457
Db 1494 TCATATTTTATCATTTTATAAAGTCTTAGTATCC-----TGCAACATA 1538
QY 1458 TATATTTATATACAGGTGCAATTAGGATGGACACACAGTAGTGTATATAGAAATTAATGCAAT 1517
Db 1539 TAAACTCAAGTGTATACGTTTGTCTTGGACACACTCTAGTGTGATCTCTTAAAAATACAA 1598
QY 1518 ATCAGATAAAATAATPACAAATGATCCAGCAATCAAGGTAAACAGTCTTTGATACAAACTC 1577
Db 1599 TTATACACATTTAACTACCCAAATTCAGCTGTAAAGCGAATTCATCTGGGACTGCTTC 1658
QY 1578 TAAGTAAATTGAGGACCTGGTCATACAGGAGGAAACTTGGTTTATTTTACAAGTCAAGG 1637
Db 1659 TAAGTTGTTTCAAGACCTGGTCATACAGGAGGGGATTTAATTTGATTTTCAAGATCA--- 1715
QY 1638 GGTTTAGAGATTACATGTAGAACTCCTTAATTTCTACACAAATCTTATTACATTAGACTTCG 1697
Db 1716 ---TTTCAAAATACATGTGCACACTCAAAATTTTCAACAATCGTATTTTATAAGAAATCG 1772
QY 1698 ATACGCTCAAAATGGTGTGGAAATACTCTTCTTAATATATCTTACAAATACCAAGGAT 1757

Db 1773 TTATCTCTCAATGGAAGCGCAAAATACACGAGCTGTTATAAATCTTAGTATCCAGGG- 1831
QY 1758 AATAGAAATACCACTCAACGACTCAACAACTTTTCTGCTAGCAAAATTAATAATTT 1817
Db 1832 --TAGCAGAACTGGGTATGGCACTCAACCCCACTTTTCTGCTACAGATTATACGAAATTT 1889
QY 1818 ACAATACGAGATTTTGGGTATTTCCAAATTTCCAAAGTACAGTAACATTACCTTTAAATCG 1877
Db 1890 AAAATATAAAGATTTTTCAGTACTTAGAAATTTTCTAACGAGGTGAATTTTGCCTCCAAATCA 1949
QY 1878 AAAATACCAATTTATATTTAATTCGTGCAGATGTAT---CAAAATTCAAATTTTAAATCATG 1934
Db 1950 AAACATATCTCTTGTGTTTAAATCGTTCGATGTATATACAAACACACACAGTACTTATTCA 2009
QY 1935 TAAATTTGAATTTATPACCAATTTACTCTCTGTACGCCAAATAATAGAGAAAAACAAATTT 1994
Db 2010 TAAATTTGAATTTTCTGCCAATTTACTCTGTTCTATAAGAGAGGATAGAGAGAAAAACAAATTT 2069
QY 1995 AGAAACTATCCAAACAAAAATAATACATTTTTCACAAATCATACAAAAATACTTTAA 2054
Db 2070 AGAAACAGTACAACAAAATAATTAATACATTTTATGCAAAATCTTATAAAAAACACTTTACA 2129
QY 2055 TATAGAGCCACAAACTATGATTTGATTA 2085
Db 2130 ATCAGAACTTACAGATTATGACATAGATCA 2160
RESULT 8
ID AAQ81178 standard; DNA; 3543 BP.
XX AAQ81178;
AC AAQ81178;
XX
DT 25-MAR-2003 (revised)
DT 12-AUG-1995 (first entry)
XX
DE B.t. toxin PS71M3 gene.
XX
KW Delta-endotoxin; crystal protein; biological control agent; Calliphoridae;
KW screw-worm; sheep blowfly; Lucilia; Phormia; Calliphora; insecticide;
KW pesticide; B.t.; ss.
XX
OS Bacillus thuringiensis.
XX
PN W09502694-A2.
XX
PD 26-JAN-1995.
XX
PF 13-JUL-1994; 94WO-US007902.
XX
PR 15-JUL-1993; 93US-00093199.
XX
PA (MYCO) MYCOGEN CORP.
XX
PI Hickie LA, Payne J;
XX
DR WPI; 1995-067338/09.
DR P-PSDB; AAR63078.
XX
PT Method for controlling Calliphoridae pests - specifically utilises
PT Bacillus thuringiensis isolates or toxins.
XX
PS Disclosure; Page 36-38; 50pp; English.
XX
CC A library was constructed from Bacillus thuringiensis PS71M3 total
CC cellular DNA in lambda Gem-11. Plasmid pMYC1625, selected in Escherichia
CC coli, contained a 8.0 kb insert expressing a beta-endotoxin gene. This
CC was sequenced (AAQ81178). A cured, acrySTALLiferous B.t. host carrying
CC pMYC1625 produced a 130 kDa crystal protein (AAR63078) toxic to
CC calliphorids. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 3543 BP; 1278 A; 566 C; 612 G; 1087 T; 0 U; 0 Other;

Query Match		15.9%;	Score 331.4;	DB 2;	Length 3543;
Best Local Similarity		53.8%;	Pred. No. 3.7e-46;	Indels 38;	Gaps 7;
Matches 856;		Conservative	0;	Mismatches 697;	
QY	499	TATAAAACGCTATTACTACCTATTTATGCGCAAGCTGCTAAATTTTCATTAAATTTATTA	558		
DB	604	TATNACATAGTATATNCTAGTTATGACAGCAGCAAACTTACATCTGACTGTATTA	663		
QY	559	CAACAAGGTGCTGAATGGCTGATGAATGGAATGCGAGATATACATCTTCCACAATTTGAA	618		
DB	664	AATCAAGCGCTCAAAATTTGAAGCGTATTTAAAAAACAATCGACAATTCGATTTTAGAG	723		
QY	619	CCTAATGCTGGACATGACTATTAATACTTTTAAAGAAATATACCTAAATAT	678		
DB	724	CCTTTGCC---AACAGCAATTTGATTTATCCAGTATGACTAAAGCTATAGAATTTAC	780		
QY	679	AGTAACTATTGTGCAAAATCCTATAGAGAAGGACTAAATAAACTTCGAAACGAACTTAAT	738		
DB	781	ACTAATATTTGCTGAACACTTATAAAAAGGATTAATTTTAAATAAAACGACGCTGAT	840		
QY	739	ATGAGATGGAGTATATTTAATGATTAATCGAAGATATATGACTATTTACTGTATTAGACT	798		
DB	841	AGTAACTCTGATGAAATATAAACTGGAACACATACATACGTATCGAAACAAAAATGACT	900		
QY	799	ATCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGATTCATAGGAAGNATAGGT	858		
DB	901	ACTGCTGATTTAGATCTTTGTGCACTCTTTCTTAATTTATGATGTAGTAAATATCCAAAT	960		
QY	859	GGCATTTAAATCTGAACCTTCAAGAGAAATTTATACAACTGAAATAAATTTTGACCGTCTT	918		
DB	961	GGTGTCAATCTGAACCTTACTCGAATAATTTAT-----CAGGTACTTAACCTCGAAGA	1013		
QY	919	ACTTACCTTGAAATTCACCCAACTCTGCTATATATGGAATATATATTTAAACAGCTTCAGGG	978		
DB	1014	AAGCCCTATAAATATTATGACTTTCAATATCAAGAGGATTCACCTACAGGTAGACCGCA	1073		
QY	979	CTTAGATATTTTCAATTTTATGATGAATTTATTTATACAAAATATGAAGTACGGG	1038		
DB	1074	TTTATTTACTTGGCTTGATTTCTTTGAATTTTATGAAAAAGCGCAAACTACTCTTAATAA	1133		
QY	1039	AATCGTTTGTGTTGCTATGCAATCGTAATAGACTCTACTT-ATGCTACGACAGGAACCTGA	1097		
DB	1134	TTTTTTCACAGCCATTAATAATGTTTTCATTACACACTTGTATTAATATATCCCAAAATC	1193		
QY	1098	AATATATATATGGAAAGAAACAGGTCCACCACACAAAAAACTTTAATACATTTGAATC	1157		
DB	1194	TAGTGTTTTGGAAATCACAATGTAACTGTATAATTTAAATCTCTGTGTTGGCAACAAA	1253		
QY	1158	CTATAAAGTTTCAATTTGTAAGTATGACAGATTAACCTCTACTCTCCCTTTTCTCAACAT	1217		
DB	1254	TATTTATATTTTATTAATAATGTATGAAGCTTAGATAATAAATATCTAAATGATTATAA	1313		
QY	1218	ATACTTTACAAATTAATCAATTTGAACCTTTATTTAATAATTCACCTAGTAAATTAATTAAC	1277		
DB	1314	TAATATTAGTAAATGGAATTTTTTATAACCTAATGCTAGACTTTTGGGAGAAGAACT	1373		
QY	1278	ATATTCAGCTGGGGGAATTTATCTAATGTATATAAAAAAACAACCTGATTTTCAATTTCCCTGT	1337		
DB	1374	TACAGCAGGATCTGGGCAAAATTAATTTATGATGTAATAAATAATTTTTCGGGTTACCAAT	1433		
QY	1338	AAAAAAGACTGTAAACCAATTTAATTCAAATTTGTTTACCAAGCTTATATAGTTAG	1397		
DB	1434	TCCTTAACCAAGAGAGAATCAAGCAATCCCTACCCCTTTTTCCAACATATGATACTATAG	1493		
QY	1398	TCATATTTTATCCAGTTTCTTTTATTTAATTTTCTTATAAATTTGGATTAGCGCTAAA	1457		
DB	1494	TCATATTTTATCATTTATTTAAAGCTTTAGTATGCC-----TGCAACATA	1538		
QY	1458	TATATTATACAGGTGCTATTAGGATGACACACAGACTAGTGTATTAAGAAATAATGCAAT	1517		
DB	1539	TAAACTCAAGTATAGCTTTTGTGTTGGACACACTCTAGTGTGATCTCTAAATAACAT	1598		
QY	1518	ATCAGATAAAATAATTAACATGATCCAGCAATCAAGGTAAACAGCTCTTGATACAAACTC	1577		
DB	1599	TTATACACATTTAACTACCCAAATTCAGCTGTAAAAAGCGAAATTCATTTGGGACTCTTC	1658		
QY	1578	TAAGGTAAATGAAGNACCTGTGCATACAGGAGAACTTTGGTTTATTTTACAAAGTCAAGG	1637		
DB	1659	TAAGGTGTGTTCAAGGACCTGGGTGCATACAGGAGGGGATTTAATTTGATTTCAAGATCA---	1715		
QY	1638	GGCTTTAGAGATTACATGTAGAACTCCTAATTTCTACACAATCTTTATTAACATTAGACTTCG	1697		
DB	1716	---TTTCAAAATTTACATGTCAACACTCAAAATTTTCAACATCGTATTTTATAAGAATTCG	1772		
QY	1698	ATACGCTCAAAATGGTGTGGAATACTCTCTCTTAATATATCTCTTACAAATACCAAGAGT	1757		
DB	1773	TTATGCTTCAAAATGGAAGCGCAAAATACACGAGCTGTTATAAAATCTTAGTATCCAGGGG-	1831		
QY	1758	AATAGAAATACCACTCAACGACTCAACAACTCTTTTCTGTGTACAAAATTAATAATTT	1817		
DB	1832	--TAGCAGAACTGGGTATGGCACTCAACCCCACTTTTCTGGTACAGATTTATAGAAATTT	1889		
QY	1818	ACAATACGGAGATTTTGGGTATTTTCCAATTTTCCAAGTACAGTAACATTTACCTTTAAATCG	1877		
DB	1890	AAATATATAAGATTTTTCAGTACTTAGAATTTTCTAACGAGGTGAAATTTTCTCCAAATCA	1949		
QY	1878	AAACATACCATTTTATATTTAATCTGTCAGATGAT---CAAATTCATTTTATCATTTGA	1934		
DB	1950	AAACATATCTCTTGTGTTTAAATCGTTTGGATGTATATACAAACACACACAGTACTTATGA	2009		
QY	1935	TAAAAATGAAATTTATACCAATTTACTTCTCTGTACGCCAAATAGAGAAAAACAAAAAT	1994		
DB	2010	TAAAAATGAAATTTTCTGCCAATTTACTCTGTTCTATAAGAGAGGTAGAGAGAAAAAAT	2069		
QY	1995	AGAACTATCCAAACAAAAATAAATACATTTTTCACAAATCATACAAAAAATACCTTTAAA	2054		
DB	2070	AGAAACAGTACAAACAAATTAATTAATCAATTTTATGCAATCTTATAAABAAACACTTTACA	2129		
QY	2055	TATGAAGCCCAACAACTATGATATTGATTA	2085		
DB	2130	ATCAGAACTTACAGATTTATGACATAGATCAA	2160		
RESULT 9					
AAD43974					
ID	AAD43974 standard; DNA; 4896 BP.				
XX	AAD43974;				
DT	13-DEC-2002 (first entry)				
DE	Bacillus thuringiensis ssp. finitimus cry28Aa1 gene.				
KW	Delta-endotoxin; cry26Aa1; cry28Aa1; insect-resistant plant; toxin;				
OS	transgenic host cell; insecticide; gene; de.				
FT	Bacillus thuringiensis.				
FT	Key Location/Qualifiers				
FT	CDS 1129..4458				
FT	/*tag= a				
FT	/product= "cry28Aa1 gene"				
PN	US2002038005-A1.				
XX	28-MAR-2002.				
XX	08-JAN-2001; 2001US-00756526.				
XX	07-JAN-2000; 2000US-0175158P.				
XX	(WOJC/) WOJCIECHOWSKA J A.				
XX	(LEWI/) LEWITIN E I.				
XX	(ZALU/) ZALUNIN I A.				
XX	(REVI/) REVINA L P.				
XX	(CHES/) CHESTUKHINA G G.				

Matches 385; Conservative 0; Mismatches 243; Indels 48; Gaps 3;

QY 153 AGGTGCTATAATAATCTTTTGGTACCTTAATCACTGTCTTTGGCCGCGGAGAAC 212
 DB 1293 AGGTGCTGCTATATATCTTTGGAACCTTGGCTCCGCTTCTTTGGCTGATCCAGAGGA 1352

QY 213 AGA---CAAACAGTAGTGGACAAATTTATTAATGGGAGAAATTTTGTGTATACACC 269
 DB 1353 AGATCCAAAATAAATTTGGTCAAAATTTATGAACACGGGAGAGACCTTTTAAATCAAC 1412

QY 270 GTTAAACAGAAAGCATAAACAGCTAAAGTTTCAAACTTTTGAAGGATTTTACAGCAATATT 329
 DB 1413 AATTTCTACAGCTGTAAGAAGATAGCATTTAGCTCTCTAAATGGTTTAAAGATGATT 1472

QY 330 ACAAAGCTATAATACAGCATTAAGATGGAGGAAATTTAAAGACTACAAAGCTCTGG 389
 DB 1473 AACGTACTATGAAGAGCAATTAATGATGGAGAGAAATCCAAAGTGCATAATCTGCCAG 1532

QY 390 ATTACCAACCATCATCAGCATTAACAACAGCTGCTTGAATCTTTAAATATAGATTGAGAA 449
 DB 1533 ATTGGTATCAAGA-----GATTTGAAA 1556

QY 450 TGTTCACAAATGATTTATTCGAGAAATACCTGGTTTCCAACTTTGAAACTTTATAAAGCCT 509
 DB 1557 CGCTCATTTCAATTTTGAAGCAATATGCCACAACCTTCCCAAGTATGACACATT 1616

QY 510 ATTACTACCTATTATGCGCAAGCTGCTAAATTTTCAATTTTAAATTTTAAACAAAGTGC 569
 DB 1617 ATTATTAAGTTGCTATACAGAGCTGCAAAATTTTACATTTTGAATTTTATACATCAAGGTG 1676

QY 570 TGAATGGCTGATGAATGGAAATGAGATATACATCTTCAAAATTCGAATTCGAATGCTGG 629
 DB 1677 ACAATTCGCGGATCAATGGAATGAGATCAACCAATTCACCAAT-----GTTGAA 1727

QY 630 AACATCAGATGACTATTATTAACCTTTTAAAGAGAAATATACCTAAATATAGTAATTTG 689
 DB 1728 GTCATCAGGACTTATTATGACGAGCTATTGGTATATATTGAAAGTATATTAATTTATG 1787

QY 690 TGCAAAATACCTTATAGAGAGGACTTAAATAAATCTTGAAGAGAACTTAAATATGAGATGGAG 749
 DB 1788 CACCAAGACATACCATTAAGATTTGAATCACTTTAAGAAATCAGAAAAATCAGATGGGA 1847

QY 750 TATATTTAAGTATTCGAAGATATATGATTAATTTACTGTTATGATATATGATCTCAATT 809
 DB 1848 TGCTTATAACACATATCGTCGAGAAATGACCTTAATTTGATTTGATCTTGTGCAACTTT 1907

QY 810 TTCTTTTATGATATA 825
 DB 1908 TCCTTTTATGATATA 1923

RESULT 11

ADP31306
 ID ADP31306 standard; DNA; 4896 BP.
 AC AC
 AC ADP31306;
 DT 12-FEB-2004 (first entry)
 XX Bacillus thuringiensis serovar finitimus pF2 DNA clone.
 DE
 XX Cry26Aa1; cry28Aa1; delta-endotoxin; insect pest control;
 KW transgenic plant; insect resistance; insecticide; gene; ds.
 XX Bacillus thuringiensis serovar finitimus.
 OS
 XX Key Location/Qualifiers
 FH 1129..4458
 CDS /*tag= a
 FT /product= "Cry28Aa1 delta-endotoxin protein"
 FT
 XX US2003154510-A1.

PD 14-AUG-2003.
 XX 15-JAN-2003; 2003US-00342821.
 PF 07-JAN-2000; 2000US-0175158P.
 PR 08-JAN-2001; 2001US-00756526.
 XX (WOJC/) WOJCIECHOWSKA J A.
 PA (LEWI/) LEWITIN E I.
 PA (ZALU/) ZALUNIN I A.
 PA (REVI/) REVINA L P.
 PA (CHES/) CHESTURKHINA G G.
 XX Wojciechowska JA, Lewitin EI, Zalunin IA, Revina LP;
 PI Chestukhina GG;
 PI WPI; 2003-897757/82.
 XX P-PSDB; ADF31307.
 DR New delta-endotoxin nucleic acid molecules, cry26Aa1 and cry28Aa1, useful
 XX for controlling insect pests and for conferring insect resistance.
 PT Claim 7; SEQ ID NO 3; 42pp; English.
 PS The present invention relates to the isolation of novel cry26Aa1 and
 XX cry28Aa1 delta-endotoxin genes from *Bacillus thuringiensis* ssp.
 CC finitimus. The sequences for the delta-endotoxin polypeptides are also
 CC disclosed. The invention provides methods for producing the toxins and
 CC compositions containing the toxins. The methods and sequences of the
 CC invention are useful for controlling insect pests in transgenic plants to
 CC confer insect resistance. The present sequence represents a DNA clone
 CC that contains the coding sequence for cry28Aa1 delta-endotoxin.
 XX Sequence 4896 BP; 1727 A; 757 C; 887 G; 1525 T; 0 U; 0 Other;
 SQ

Query Match 7.7%; Score 161.2; DB 10; Length 4896;
 Best Local Similarity 57.0%; Pred. No. 8.9e-18;
 Matches 385; Conservative 0; Mismatches 243; Indels 48; Gaps 3;

QY 153 AGGTGCTATAATAATCTTTTGGTACCTTAATCACTGTCTTTGGCCGCGGAGAAC 212
 DB 1293 AGGTGCTGCTATATATCTTTGGAACCTTGGCTCCGCTTCTTTGGCTGATCCAGAGGA 1352

QY 213 AGA---CAAACAGTAGTGGACAAATTTATTAATGGGAGAAATTTTGTGTATACACC 269
 DB 1353 AGATCCAAAATAAATTTGGTCAAAATTTATGAACACGGGAGAGACCTTTTAAATCAAC 1412

QY 270 GTTAAACAGAAAGCATAAACAGCTTAAAGTTTCAAACTTTTGAAGGATTTTACAGCAATATT 329
 DB 1413 AATTTCTACAGCTGTAAGAAGATAGCATTTAGCTCTCTAAATGGTTTAAAGATGATT 1472

QY 330 ACAAAGCTATAATACAGCATTAAGATGGAGGAAATTTAAAGACTACAAAGCTCTGG 389
 DB 1473 AACGTACTATGAAGAGCAATTTAATGATGGAGAGAAATCCAAAGTGCATAATCTGCCAG 1532

QY 390 ATTACCAACCATCATCAGCATTAACAACAGCTGCTTGAATCTTTAAATATGAGATTGAGAA 449
 DB 1533 ATTGGTATCAAGA-----GATTTGAAA 1556

QY 450 TGTTCACAAATGATTTATTCGAGAAATACCTGGTTTCCAACTTTGAAACTTTATAAAGCCT 509
 DB 1557 CGCTCATTTCAATTTTGAAGCAATATGCCACAACCTTCCCAAGTATGACACATT 1616

QY 510 ATTACTACCTATTATGCGCAAGCTGCTAAATTTTCAATTTTAAATTTTAAACAAAGTGC 569
 DB 1617 ATTATTAAGTTGCTATACAGAGCTGCAAAATTTTACATTTTGAATTTTATACATCAAGGTG 1676

QY 570 TGAATGGCTGATGAATGGAAATGAGATATACATCTTCAAAATTCGAATTCGAATGCTGG 629
 DB 1677 ACAATTCGCGGATCAATGGAATGAGATCAACCAATTCACCAAT-----GTTGAA 1727

QY 630 AACATCAGATGACTATTATTAACCTTTTAAAGAGAAATATACCTAAATATAGTAATTTG 689

1142 TAATACCAATTTGAATCCTTAAGTTTCAATTTGTAATCTGATAGACAAAGTAACCTCTACTT 1201
1178 TTTCTCAAGACACATCCAAAGTATTTCCCTTTTATAGAAACAAACCTATTGTAAGGTGG 1237
1202 CCCCTTTTCTTAACATATACCTTTACAAATTAATCAAAATTCGAATTTTATTAATAATTTAC 1261
1238 AAATTGTCAGACATAGAGAGTACTCAGATATATATATATATATATATATATATATATATATAT 1297
1262 CTAGTAATAAATTAACATATTCAGCTGGGGGAATTTATCTAATGATATAAAAAACAACCTG 1321
1298 GCAGTGAAGTATTTTCGATATTCATCCAAATTCACAAATAGAAAATAATATATAAAGAACTG 1357
1322 ATTTTCAATTTCTGTATAAATAAGACTGTAAACCAATTAATCAAAATTTGTTTACCA 1381
1358 ATTTTATATGATTTCCAAAACAACATGGAATAATTAAGAAATATGCTACTATCTATCGT 1417
1382 GCTATATATAGTTATAGTTCATATTTTATCCAGTTTCTTTATTTAATTTATCTCTATAAAA 1441
1418 ATATAAAACTTGATAATTTATATTTTC----- 1445
1442 TTGGATTAGCGCTAAATATATATATATATACAGGTGCATTTAGAGTGGACACACAGTAGTGTAA 1501
1446 -----AGTAGTTAGAGAGAGAGAGAGTTGCAATTTAGTTGACACATACACTAGTGTG 1498
1502 ATAGAAATATGCAATATACATGATAAATAATTAATTAATGATCCAGCAATCAAAAGGTAA 1561
1499 ATTTCCAAAATACAAATAGATTTAGATAACATCAACCAATCCACGCTCTAAAGCTTTGA 1558
1562 GTCTTGATCAAACTCTAGGTAAATTCAGGACCTGTCTATACAGAGGAACTCTGTTT 1621
1559 AGTAAAGTTCTGATTCGAAATTTGAAAGGTCCTGTCTACACAGGTGGAGCTTGGTAA 1618
1622 ATTTCAAAAGTCAAGCGCTTTAGAGATTAATCATGTAGAACTCCCTAAATTTTACAAATCTT 1681
1619 TTCTTAAGTAGTAGTGGATTTAGAGTTAGATTTTAAATAATGTTTCTCGCAAT--- 1675
1682 ATTTACATTTAGACTTCGATACGCTACAAATGGTGTGGAATATCTTCTCTAATATATCTC 1741
1676 ATCAAGTACGTAATTCGTTATGCTACTAATGCTCCAAAGACACACAGTA--TTCTTAACCGG 1733
1742 TTACAATACAGAGTAATAGGAATACCACTCAAGCTCAACACACACATTTTCTTGTA 1801
1734 AATAGATACTATAAGTGTGGAGCTCCCTAGTACACTTCCCGCCAAAC-----C 1783
1802 CAAATTAATAATTTTACAATACGAGATTTTGGGTATTTCCAAATTTCCAAAGTACAGT-- 1859
1784 CAAATGCTACAGATTTTAAATATGCAATTTGGATATGTAATTTCCAAAGACAGTTC 1843
1860 -----AACATTACCTTTTAAATCGAAACATACCAATTTATTTAATTCGTCGAGATGTAT 1912
1844 CAAATAAACAATTTGAAGGAGAGACACTTTTATTAATGACCTTATATGTTGACACCAATC 1903
1913 CAAATTCAAATTTAATCATGATAAATTTGAATTTATATACCAATTTACTTCTCTGACGCC 1972
1904 ATTCATATATATATATTTGACAAATTCGAATTTATTCGAATCCTCAATCTGTATAG 1963
1973 AATAAGAGAAACAAATAATTTAGAACTATCCAAACAAATAAATAATATATTTTTCACAA 2032
1964 ATTTACAGAGACCAATAATATAGAAAACACAGAAAATAGTGAATGATTTATTTGTTA 2023
2033 ATCATACAAAATAATCTTTTAAATATAGA 2060
2024 ATTAACAAAGTTCTTACTAAATATAGA 2051

RESULT 13
AAQ81180
ID AAQ81180 standard; DNA; 2061 BP.

XX AC AAQ81180;

DT 25-MAR-2003 (revised)

12-AUG-1995 (first entry)
XX DE B.t. toxin PS7IM3 gene.
XX KW Delta-endotoxin; cryetal protein; biological control agent; Calliphorid;
KW screw-worm; sheep blowfly; Lucilla; Phormia; Calliphora; insecticide;
XX KW pesticide; B.t.; ss.
XX OS Bacillus thuringiensis.
XX PN W09502694-A2.
XX PD 26-JAN-1995.
XX PF 13-JUL-1994; 94WO-US007902.
XX PR 15-JUL-1993; 93US-00093199.
XX PA (MYCO) MYCOGEN CORP.
XX PI Hickie LA, Payne J;
XX DR WPI; 1995-067338/09.
XX DR P-PSDB; AAR63079.
XX PT Method for controlling Calliphoridae pests - specifically utilises
XX Bacillus thuringiensis isolates or toxins.
XX PS Disclosure; Page 42-43; 50pp; English.
XX CC A library was constructed from Bacillus thuringiensis PS7IM3 total
XX cellular DNA in lambda Gem-11. Plasmid pMYC1636, selected in Escherichia
XX coli, contained a 15 kb insert expressing a beta-endotoxin gene. This was
XX sequenced (AAQ81180). A cured, acrystalliferous B.t. host carrying
XX pMYC1636 produced a 77 kDa crystal protein (AAR63079). (Updated on 25-MAR
XX -2003 to correct PN field.)
SQ Sequence 2061 BP; 779 A; 331 C; 319 G; 632 T; 0 U; 0 Other;

Query Match 7.6%; Score 158; DB 2; Length 2061;
Best Local Similarity 48.3%; Pred. No. 3e-17;
Matches 999; Conservative 0; Mismatches 895; Indels 174; Gaps 13;

QY 2 TGTGTCGAAGGAATACACAAATATGTCATATATTCGAGACATTTGCTAGTCTGATACAA 61
DB 149 TGTGTCGAAGGAATACACAAATATGTCATATATTCGAGGAATTTGTTAGTCTGAACTA 208
QY 62 TTGCTGCAGTTAGTGCAGGTACTATTGTTATCCGGTACTCTGTTAGCCGGTATAGGTGGC 121
DB 209 TTGTTGGAGTTAGTGCAGGTATTATTGTTAGTAGGAACATATGTTAGGAGCTTTTCTGCC 268
QY 122 TCACCTTCTATATCCGGNCCGATAGGAATATAGTCTATAATAATATCTTTTGGTACCC 181
DB 269 -----CTGCTTTCGAGGTATAATATCTTTTGGACTT 304
QY 182 TAATCACTGTCTTTTGGCCCGCGGAGAACAAAGACATATGTCAGACAAATTTTATTA 241
DB 305 TGTTCGCGATCTTTTGGCAAGGATCTGACCTG---CAAATGTTTGGCAGGATTTGTTAA 361
QY 242 AAATGGGAGAAATTTTGTGTTGATACACCGTTTAAACAGAAAGCATAAAACAGCTAAGTTAC 301
DB 362 ACATCGGAGGAGCCCTATACAGAAATAGATAAAACATAAATTAATGTAACACTT--- 418
QY 302 AAATTTAGAGGATTTTGTAGCAAAATATACAAAGCTATATACAGCATTAGATGATGGA 361
DB 419 ---CTATCGTAACACCTTATAAATAATCAACTTGTATAAATCAAGAATTTTTCGATAAAT 475
QY 362 GAAATTTAAAGACTCAAGCTCCTGGATTACCACTATCATCAGCATTTACAAAGCTG 421
DB 476 GGGAGCCAGCAGCTACACAGCTAATGCTAAAGCAGTA-CATGATCTCTTTTACTACCTTA 534
QY 422 CTTTGACTCTTAAATATCGATTTGAGAAATGTTCAATGATTTTATTCGAGAAATACCTG 481

Db 535 GAACCTATTAATAGATTAAGATTAGATATGTTAAAAA----- 571
Qy 482 GTTTCAACTTGAACTTATAAAGCTTATTACTACCTATTTATGCGCAAGCTGCTAATT 541
Db 572 -----ATAATGCTAGCTATCGAATACCAACACTCCCTGCATATGCACAAATAGCTACTT 625
Qy 542 TTCAATTAAATTTATACAAAGGCTGGAATTTGGCTGATGAATGGAATGCAGATATAC 601
Db 626 GGCACCTGAATTTATTAACAACATGCTGCTACCTATTAACAATATATGCTGCAAAATCAAG 685
Qy 602 ATCCCTTCAAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATAAACTTTTAAAG 661
Db 686 GT-----ATAATCCAGTACTTTCAATTCATCTAATTTACTATCAGGCTATTTAAC 739
Qy 662 AAAATATACCTAAATATAGTAATTTGGCAAAATACCTATAGAGAAAGGACTAAATAAAC 721
Db 740 GTAAAAATACAAGATATAGTACTATGTTATACAAACGTACAAATGCAGGACTAACTATGA 799
Qy 722 TTGCAACGAACTTAATATGAGATGGAGTATATTTAATGATTTATCGAAGATATATGACTA 781
Db 800 TTAGAACTTAATACTAACGCAACATGGAATATGTAATAATACTTACCGTTTATAGAAATGACTC 859
Qy 782 TTACTGTATTAGATACTATCGCTCAATTTTCTTTTATGATATAAGAGATACAAAGATT 841
Db 860 TAACTGTGTAGTACTTATGCTATTGCTATTTTCCAAATTTATGACCCAGAAAATA----- 911
Qy 842 CAATAGGAAGATAGGTGGCATTTAAACTGAACCTTACAAGAGAAATTTATACAACCTGAA 901
Db 912 -----TCCAAATAGGAGTTAAATCTGAACCTTACCAGAGAAGTTTATACGAATGTTA 961
Qy 902 TAAATTTTGACCGTCTTACTTACTTGAATTTCAACCCCAATCTCGCTATAATGGATATA 961
Db 962 -----ATTGAGTATACATTTTAGAACCAATAACAGAACTAGAAA 997
Qy 962 ATTTAACAGCTTCAGGCTTAGATTATTTTCAATTTTATAGTCAACTTATATTTTATACAA 1021
Db 998 ATGGATTAACTAGAAATCTCATATTATTTTCTGGATAAACCAAGGCGTTTATACACNA 1057
Qy 1022 AAAATGAAACGTACGGGAATCGTTTAGTTGGTATTGCGAATCGTAAATAGATCTACTATTG 1081
Db 1058 GAAATCTCGACACATCTCTGTATCTGATGATATTTTCTTTTACAGGTACCCAGATGG 1117
Qy 1082 CTACGACAGGAATGAAATATATATGGAGAAGAACAGGTCACCCCAACAAACAACTT 1141
Db 1118 CTTTACACATATAATGATATGATCGCAACATAATCTGGGGAGCGTTTCATGACATATTA 1177
Qy 1142 TAAATACCACTTTCGATCTTAAAGTTTCAATTTGTAACCTGATAGACAAAGTAACTCCTACTT 1201
Db 1178 TTTCTCAAGACACATCCAAAGTATTTCCTTTTATAGAAAACAACTTATGTAAGGTCTG 1237
Qy 1202 CCCCTTTTCTAACATATATCTTACAATTTAATCAAAATGAACTTTTATTTAAATAATTCAC 1261
Db 1238 AAATTTGTCAGACATAGAGAGTACTCAGATATAATATATGAAATGATATTTTTCGAATA 1297
Qy 1262 CTAGTAATAAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATAAAAAACAACTG 1321
Db 1298 GCAGTGAAGTATTTGATATTTTTCGATTTTTCATCAATTCACAAATAGAAAATTAATATAAAAGAACTG 1357
Qy 1322 ATTTTCAATTTCTGTAATAAAGAACTGTAAACCAATTTAATCCAAATTTGTTTACCAA 1381
Db 1358 ATCTTTATATGATTTCCAAAACAAACATGGAANAANTAAAGAATATGGTCATCTCTATCGT 1417
Qy 1382 GCTATAATATAGTTATAGTCATATTTTATCCAGTTTTCCTTTTATTTAATTTCTCTATAAA 1441
Db 1418 ATATAAAACTGATAATATATATTTTC----- 1445
Qy 1442 TTGGATTACGGCTAAATATATTTATATACAGGTGCTTAGGATGGACACACTAGTGTGA 1501
Db 1446 -----AGTAGTTAGAGAAGAAGAAGAGTTGCAATTTAGTTGGACACATCTAGTGTG 1498
Qy 1502 ATAGAAATATGCAATATCAGATAAAATTAATTTACAAATGATCCAGCAATCAAAAGGTAAACA 1561
Db 1499 ATTTCCAAATACATAGATTTAGATATACATCACCCCAATCCACGCTCTAAAGCTTTGA 1558

Qy 1562 GTCCTGATACAAACTCTAAGGTAAATTTGAAGNCCTGGTCTATACAGAGGAAACTTTGGTTT 1621
Db 1559 AGGTAAGTTCTGATTCGAAAATTTGTGAAGGTCCTGGTGCACACAGGTGGAGACTTTGGTAA 1618
Qy 1622 ATTTCAAAAGTCAAGGGCGTTTAGAGATTACATGTAGAACTCCTAATCTACACAACTTT 1681
Db 1619 TCTTAAAGATAGTATGGAATTTTAGAGTTAGATTTTAAANAATGTTTCTCCACAAT--- 1675
Qy 1682 ATTACATTTAGACTTCGATACGCTACAAATGCTGGGAAATATCTTCTCTAATATATCTC 1741
Db 1676 ATCAAGTACGTATTCGTTATGCTACTAATGTCTCCAAAGACACACAGTA--TTCTTAACCGG 1733
Qy 1742 TTACAAATACCAGGAGTAAATAGGAATACCACCTCAAGGACTCAACACACTTTTCTCGGTA 1801
Db 1734 AATAGATACTATAAGTGTGGAGCTCCCTAGTACCACTTCCCGCCAAAAC-----C 1783
Qy 1802 CAAATTAATAAATTTTACAATACGAGATTTTGGGTATTTCCAAATTTCCAAGTACAGT-- 1859
Db 1784 CAAATGCTACAGATTTAATACATATGCGATTTTGGATATGTAACATTTCCAAGAACAGTTC 1843
Qy 1860 -----AACATTACCTTTAAATCGAAACATACCACTTTTATATTTAATCGTGCAAGATGAT 1912
Db 1844 CAAATAAAACATTTGAAGGAGAGACACTTTTATTAATGACCTTATATGTCACACCAAAATC 1903
Qy 1913 CAAATTCATTTTAAATCATTTGATAAAATTTGAATTTTATACCAATTTCTCTCTGACGCC 1972
Db 1904 ATTCATATAATATATATATTTGACAAAATCGAATTTTATTTCCAAATCACTCAATCTGTATTAG 1963
Qy 1973 AAAATAGAGAAAACAAAAATTTAGAAACTATCCAAACAAAATAAATAATACATTTTTCACAA 2032
Db 1964 ATTATACAGAGAGCAAAATATAGANAANAACAGAGAAATAGTGAATGATTTATTGTTA 2023
Qy 2033 ATCATACAAAANAATCTTTTAAATATAGA 2060
Db 2024 ATTTAAACAAAGTTCTTACTAAATAGA 2051

RESULT 14

AAN50525

ID AAN50525 standard; DNA; 3756 BP.

XX AAN50525;

AC AAN50525;

XX 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 23-OCT-1991 (first entry)

XX Bacillus thuringiensis var. israelensis endotoxin insert in plasmid

DE PSY367.

XX Endotoxin; insecticide; ss.

KW Bacillus thuringiensis serovar israelensis.

OS Bacillus thuringiensis serovar israelensis.

XX EP153166-A.

PN 28-AUG-1985.

XX 15-FEB-1985; 85EP-00301017.

PF 22-FEB-1984; 84US-00582506.

PR 22-JAN-1985; 85US-00693556.

XX (SYTR) SYNTRO CORP.

XX Walfield AM, Pollock TJ;

XX WPI; 1985-211724/35.

XX Polypeptide active against Diptera insects - prepd. from DNA sequence

PT coding for BTI endotoxin using bacterial host.

XX

PS Disclosure; Page 15a-e; 27pp; English.

XX The B. thuringiensis var. israelensis endotoxin insert in pSV367 is
CC expressed in a bacterial host. The protein produced has insecticidal
CC activity against dipteran insects. (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 24-OCT-2003 to standardise OS field)

XX
SQ Sequence 3756 BP; 1379 A; 566 C; 659 G; 1150 T; 0 U; 2 Other;

Query Match 7.1%; Score 148.2; DB 1; Length 3756;
Best Local Similarity 48.3%; Pred. No. 1.3e-15;
Matches 1001; Conservative 0; Mismatches 893; Indels 177; Gaps 14;

QY 2 TGTGTCAGGGAATACACATATGCTGATATTCGAGACATTTGCTAGTCTGATACAA 61
DB TGTGTCAGGGAATACACATATGCTGATATTCGAGACATTTGCTAGTCTGATACAA 1148

QY 62 TTGCTGCAGTTAGTCAGGCTACTTGTATCCGCTACTCTGTTAGCCGGTATAGTGGGC 121
DB TTGCTGCAGTTAGTCAGGCTACTTGTATCCGCTACTCTGTTAGCCGGTATAGTGGGC 1208

QY 122 TCACCTTTATATCCGACCGATAGGAATAATAGTGTCTATAATAATCTTTTGTACCC 181
DB TCACCTTTATATCCGACCGATAGGAATAATAGTGTCTATAATAATCTTTTGTACCC 1244

QY 182 TAATCACTGTCTTTTGGCCCGGGAGAAACAGACAAAACAGTATGACACAAATTTATTA 241
DB TAATCACTGTCTTTTGGCCCGGGAGAAACAGACAAAACAGTATGACACAAATTTATTA 1301

QY 242 AATGGGAGAAATTTTGTGTTGATACACCGTTTACAGAAAGCATAAAACAGCTAAAGTTAC 301
DB AATGGGAGAAATTTTGTGTTGATACACCGTTTACAGAAAGCATAAAACAGCTAAAGTTAC 1358

QY 302 AAACCTTTAGAGGATTTAGACAAATATTACAAAGCTATAATACAGCAATTAGATGGA 361
DB AAACCTTTAGAGGATTTAGACAAATATTACAAAGCTATAATACAGCAATTAGATGGA 1415

QY 362 GAAAATTTAAAGACTACAGCTCCTGGATTACACACCATCATGCAATTAACAAAGCTG 421
DB GAAAATTTAAAGACTACAGCTCCTGGATTACACACCATCATGCAATTAACAAAGCTG 1474

QY 422 CCTTGACTCTTAAATACGATTTGAGAAATGTTCAATGATTTTATTCGAAATACCTG 481
DB CCTTGACTCTTAAATACGATTTGAGAAATGTTCAATGATTTTATTCGAAATACCTG 1511

QY 482 GTTTTCCAACTTTGAAACTTTATAAAACGCTATTACTACTCTATTATTCGCAAGCTCTAATT 541
DB GTTTTCCAACTTTGAAACTTTATAAAACGCTATTACTACTCTATTATTCGCAAGCTCTAATT 1565

QY 542 TTCAATTTAAATTTATTAACAAGGCTGTAATTTGGCTGATGAATGGAAATGCAGATATAC 601
DB TTCAATTTAAATTTATTAACAAGGCTGTAATTTGGCTGATGAATGGAAATGCAGATATAC 1625

QY 602 ATCCTTCACAAATTTGAACCTTAATGCTGGAACATCAGATGACTATTATAAACTTTTAAAG 661
DB ATCCTTCACAAATTTGAACCTTAATGCTGGAACATCAGATGACTATTATAAACTTTTAAAG 1679

QY 662 AAAATATACCTTAAATATAGTAACTATTGTGCAAAATACCTATAGAGAAGGACTAAATAAAC 721
DB AAAATATACCTTAAATATAGTAACTATTGTGCAAAATACCTATAGAGAAGGACTAAATAAAC 1739

QY 722 TTCGAAACGAAACCTTAATAATAGATGGAGTATTTTAAATGATTAATCGAAGATATATGACTA 781
DB TTCGAAACGAAACCTTAATAATAGATGGAGTATTTTAAATGATTAATCGAAGATATATGACTA 1799

QY 782 TTACTGTATTAAGATCTATCCCTCAATTTTCTTTTATGATATAAAGATACAAAGATT 841
DB TTACTGTATTAAGATCTATCCCTCAATTTTCTTTTATGATATAAAGATACAAAGATT 1851

QY 842 CAATAGGAAGAATAGGTGGCAATTTAAACCTGAACCTTTACAGAGAAATTTATACAACTGAAA 901
DB CAATAGGAAGAATAGGTGGCAATTTAAACCTGAACCTTTACAGAGAAATTTATACAACTGAAA 1901

QY 1852 -----TCCATAGGAGTTAAATCTGAACCTTATCAGAGAGGTTTATACGATGTTA 1901

QY 902 TAAATTTTGACCGTCTTACTTACCTTGAATAATCAACCCCAATCTCGCTATAATGGAATATA 961
DB TAAATTTTGACCGTCTTACTTACCTTGAATAATCAACCCCAATCTCGCTATAATGGAATATA 1937

QY 962 ATTAAACAGTTTCAGGGCTTAGATTTATTTTTCATTTTATAGTGAACCTTATTTTATACAA 1021
DB ATTAAACAGTTTCAGGGCTTAGATTTATTTTTCATTTTATAGTGAACCTTATTTTATACAA 1997

QY 1022 AAAATGAAACGTACGGGAATCGTTTGTAGTTGATTCGGAATCGTAATAGATCTACTTATG 1081
DB AAAATGAAACGTACGGGAATCGTTTGTAGTTGATTCGGAATCGTAATAGATCTACTTATG 2057

QY 1082 CTACGACAGAACTGAAATTTATATATGAGAGAAAGACAGCTCCACCCACAAACAACTT 1141
DB CTACGACAGAACTGAAATTTATATATGAGAGAAAGACAGCTCCACCCACAAACAACTT 2117

QY 1142 TAATACCATTTGATCTTAAAGTTTCAATTTGTAATCTGATGACAGTAAGTCTCTACTT 1201
DB TAATACCATTTGATCTTAAAGTTTCAATTTGTAATCTGATGACAGTAAGTCTCTACTT 2177

QY 1202 CCCCTTTTCTTAACATATATCTTTACAAATTAATCAAAATTTGAACTTTATTTAAATAATTCAC 1261
DB CCCCTTTTCTTAACATATATCTTTACAAATTAATCAAAATTTGAACTTTATTTAAATAATTCAC 2237

QY 1262 CTAGTAAATTAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATAAAAAACAACTG 1321
DB CTAGTAAATTAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATAAAAAACAACTG 2297

QY 1322 ATTTTCAATTTCTGTAATAAAAAAGACTGTAAACCAATTTAATCCAAATTTGTTTACCA 1381
DB ATTTTCAATTTCTGTAATAAAAAAGACTGTAAACCAATTTAATCCAAATTTGTTTACCA 2357

QY 1382 GCTATTAATAGTTATGCTATTTTATCCAGTTTCTTTTATTTAATTTATTTCTTATAAAA 1441
DB GCTATTAATAGTTATGCTATTTTATCCAGTTTCTTTTATTTAATTTATTTCTTATAAAA 2385

QY 1442 TTGGATTTAGCGCTTAAAT 1501
DB TTGGATTTAGCGCTTAAAT 2438

QY 1502 ATGAAATTAATGCAATATCAGATAAATAATTAATTAATGATCCAGCAATCAAGGTAACA 1561
DB ATGAAATTAATGCAATATCAGATAAATAATTAATTAATGATCCAGCAATCAAGGTAACA 2498

QY 1562 GTCTTGATACAACTCTTAAGTAAATGCAAGGCTGCTCATACAGGAGGAACTTTGGTTT 1621
DB GTCTTGATACAACTCTTAAGTAAATGCAAGGCTGCTCATACAGGAGGAACTTTGGTTT 2558

QY 1622 ATTTACAAAGTCAAGGCGTTTATAGAGATTACATGTAGAACTCTCTAAATTTCTACAACTTT 1681
DB ATTTACAAAGTCAAGGCGTTTATAGAGATTACATGTAGAACTCTCTAAATTTCTACAACTTT 2615

QY 1682 ATTACATATAGACTTCGATACGCTTACAAATGGTGTGGAATACTCTTCTTAATATATCTC 1741
DB ATTACATATAGACTTCGATACGCTTACAAATGGTGTGGAATACTCTTCTTAATATATCTC 2673

QY 1742 TTACAAATCAGGAGTAATAGGAATACCACTCAACGACTCAACAACTCTTTTCTGCTA 1801
DB TTACAAATCAGGAGTAATAGGAATACCACTCAACGACTCAACAACTCTTTTCTGCTA 2723

QY 1802 CAAATTAATAATTAATAACAATACGAGATTTGGGTAATTTCCAAATTTTCCAAAGTACAGT-- 1859
DB CAAATTAATAATTAATAACAATACGAGATTTGGGTAATTTCCAAATTTTCCAAAGTACAGT-- 2783

QY 1860 --AATTTTAAATCGAAACATACCAATTTATA-----TTTAAATCGTCGAGATG 1909
DB --AATTTTAAATCGAAACATACCAATTTATA-----TTTAAATCGTCGAGATG 2843

QY 1910 TATCAATTTCAATTTTAAATCAATTTGATTAATTAATGAAATTTATACCAATTTCTCTCTGAC 1969
DB TATCAATTTCAATTTTAAATCAATTTGATTAATTAATGAAATTTATACCAATTTCTCTCTGAC 2903

QY 1970 GCCAAATAGAGAAAAACAAAAATAGAAACTATCCAAACAAAAAATAAATACATTTTTC 2029

Db	2904	TAGATTATACAGAGAACCAAAATATAGAAAAACACAGAAATAGTGAATGATTATTG	2963
Qy	2030	CAAAATCATACAAAAATACCTTTAAATATAGA	2060
Db	2964	TTAAATTAAACAAGTTCTTACTAAATAGA	2994
RESULT 15			
ID	ABL34155/c		
XX	ABL34155 standard; DNA; 15548 BP.		
AC	ABL34155;		
XX			
DT	26-MAR-2002 (first entry)		
XX			
DE	Human immune system associated gene SEQ ID NO: 2128.		
XX			
KW	Human; immune system disease; cytosine methylation; antiasthmatic;		
KW	antiarteriosclerotic; antianaemic; cytosatic; nootropic;		
KW	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;		
KW	antiinflammatory; antiarthritic; antidiabetic; antipsoriatic;		
KW	antiflammatory; cancer; eye disease; arteriosclerosis; anaemia;		
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;		
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;		
db.			
XX			
OS	Homo sapiens.		
XX			
XX	WO200200928-A2.		
PN			
XX			
PD	03-JAN-2002.		
XX			
XX	02-JUL-2001; 2001WO-EP007537.		
PF			
XX			
PR	30-JUN-2000; 2000DE-01032529.		
PR	01-SEP-2000; 2000DE-01043826.		
XX			
PA	(EPIG-) EPIGENOMICS AG.		
XX			
PI	Olek A, Piepenbrock C, Berlin K;		
XX			
DR	WPI; 2002-130909/17.		
XX			
PT	Nucleic acid comprising fragment of chemically modified gene, useful for		
PT	diagnosis and treatment of diseases associated with abnormal cytosine		
PT	methylation.		
XX			
PS	Claim 1; SEQ ID NO 2128; 32pp + Sequence Listing; German.		
XX			
CC	The present invention provides a number of human immune system associated		
CC	genes which are modified by the methylation of cytosines. The sequences		
CC	can be used in the diagnosis and treatment of immune system disorders,		
CC	including eye diseases such as retinopathy, neovascular glaucoma and		
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid		
CC	leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,		
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel		
CC	diseases. The present sequence is a gene of the invention		
XX			
SQ	Sequence 15548 BP; 4209 A; 247 C; 2903 G; 8189 T; 0 U; 0 Other;		
Query Match			
Best Local Similarity 5.6%; Score 117; DB 6; Length 15548;			
Matches 819; Conservative 0; Mismatches 1040; Indels 18; Gaps 6;			
Qy	218	AAACGCTATGGACACATTTTAAATGGAGAAATTTTGGTGTATACACCGTTAACAG	277
Db	13398	ATAAAATATACACGCATAAAATATATACGTATAAAATATATATATAAAATATACACGT	13339
Qy	278	AAAGCATAAAACAGCTAAAGCTTACAACTTTTAGAAGGATTTAGACAAATATTACAAAGCT	337
Db	13338	CTAAATATATATATATAAAATATTCCCGTATAAAATATATATCTAAATATATATAT	13279

Qy	338	ATAATACAGCATTAGATGATTTGGAGAAATTTAAAGACTACAAAGCTCCTGGATTACCAC	397
Db	13278	AAAATATATATCTAAAAATATATATAAAATATATATCTAAAAATATATATATAATAA	13219
Qy	398	CATCATCAGCATTACAAACAAGCTGCCTTGACCTCTTAAAAATAGGATTTGAGAATGTT	457
Db	13218	TATATCTAAAAATATATATATAAAATATATATCTAAAAATATATATAAAATATATAT	13159
Qy	458	ATGATTTTATTCGAGAAATACCTGGTTTCCAACTCTGGAACCTTATAAAACGCTATTACT	517
Db	13158	TAAAAATATATATATAAAATATATATCTAAAAATATATATATAAAATATATATAAA	13099
Qy	518	CTATTTATCGCGCAAGCTGCTAATTTTCATTTTAAATTTTATTACAAACAAGGTGCTGA	577
Db	13098	ATATATATATATAA--AATATATAAAATATATATATAAAATATATATAATATATACA	13042
Qy	578	CTGATGAATGGAATGCAGATACATACCTTCCAAAATTCGAACCTAATGCTGGAACATCAG	637
Db	13041	TACATATATAAAATATATATATAACAATATACATATATAAAATACATATATACAATAT	12983
Qy	638	ATGACTATTATATAAATCTTTTAAAAAGAAATATACCTTAAATATATAGTAACTATTGTG	697
Db	12982	ATATAAAATATATATAAAATATATATAAAATATATATAATAATATATATATACGAAAT	12923
Qy	698	CCTATAGAGAGGACTAAATATAAATCTTCGAAACGAACCTTAATATGAGATCGAGTATAT	757
Db	12922	TATATATACGAAATATATATAATATATATATACGAAATATATATATACGAAATATATA	12863
Qy	758	ATGATTATCGAAGATATATGACTATTCTGTATTAGATACTATCGCTCAATTTTCTTTT	817
Db	12862	TAAATATATACGAAATATATATATACGAAATATATATAATATATATAATATATATAT	12803
Qy	818	ATGATATATAAGAGATACAAAGATTCATAGGAAGAAATAGGTGGCATTAACACTGAACTTA	877
Db	12802	ACGAAATATATATACGAAATATATATAATAATATATATAATAATAATAATAATAACGAA	12743
Qy	878	CAAGAGAAATTTATACAACTGAAATAAAATTTTGACCGTCTTACTTACCTTGAAATTCAC	937
Db	12742	TATATATATAATATATATAAAATATATATATA--CGAAATATATATAAATATATATAT	12684
Qy	938	CCAATCTCGCTATAATGGAATATAATTTAAACAGTTTCAGGGCTTAGATTATTTCATTTT	997
Db	12683	AAAATATATATACGAAATAAATATAATATAATATATAATAAAATATATATACGAAATA	12624
Qy	998	TAGATGAAT--TATATTTTATACAAAAATGAAACGTACGGGAATCGTTTAGTGTATT	1056
Db	12623	TATATAATAATATATATAACATATATACATAAAATATATATAATAATAATAATAATA	12564
Qy	1057	GGCAATCGTAATAGATCTACTTTATGCTACGACAGGAACCTGAAATTTATATATGAGAAAGA	1116
Db	12563	TAAATATATATATATAAAATATATACATAAAATATATATAATAATAATAATAATAATA	12504
Qy	1117	ACAGGTCCACCACCAACAAAAACTTTTA-----ATACCATTTTGAATCCTATAAAGTT	1167
Db	12503	ATATATATATAAAATATATACATAAAATATATATAATAAAATATATACATAAAATAT	12444
Qy	1168	TCAATTTGTAATGATAGACAAAGTAACTCTACTTCCCTTTTCCCTTAAACATATCTTACA	1227
Db	12443	ATATATAAACATATATACATAAAATATATATAATAACATATATACATAATAACATATAT	12384
Qy	1228	ATTATCAAAATGAACTTTTATTAATAATTTCACTAGTAAATAATTAACATATTCAGCT	1287
Db	12383	ATATAACATATATATATAACATATATATAACATATATATAACATATATATAACATATAT	12324
Qy	1288	GGGGGGAATTTTCTAAATGATAAAAAACAACCTGATTTTCAATTTTCTCTGTAAAAAAGAC	1347
Db	12323	AACATATATATAACATATATATAATAACATATATATAATAACATATATATAAACA	12264
Qy	1348	TGTAAACCAATTTTAAATCCAAATTTGTTTACCAAGCTATAAGTATTAGTCAATTTTA	1407
Db	12263	TATATATATAACATATATATAAACAATATATATAATAACATATATATAAACAATATA	12204
Qy	1408	TCCCAGTTTTCCTTTATTAA---TTATTCTATAAAATTTGGATTAGCGCTAAATATATTA	1464

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Result No.	Score	Query		Length	DB	ID	Description
		Match	Star				
C 1	100	4.8	2157	10	CL081966	CL081966	CH216-165
C 2	98.4	4.7	1758	10	CL509408	CL509408	SAIL 811
C 3	95.2	4.6	1981	10	CL082000	CL082000	CH215-165
C 4	90.2	4.3	1392	10	CG757503	CG757503	P052-4-C0
C 5	90.4	4.3	1539	10	AG340947	AG340947	Mus muscu
C 6	90	4.3	1896	10	AG735083	AG735083	P049-1-C0
C 7	89.4	4.3	1542	10	AG386981	AG386981	Mus muscu
C 8	88.8	4.3	1608	10	CL118721	CL118721	ISB1-72J8
C 9	88.4	4.2	1489	10	AG350139	AG350139	Mus muscu
C 10	87.2	4.2	734	10	CNS010MP	AL099183	Drosophi
C 11	86.8	4.2	1348	10	CG749499	CG749499	P043-4-A0
C 12	86	4.1	1101	10	CNS00EVL	AL069706	Drosophi
C 13	85	4.1	1391	10	CG754863	CG754863	P050-2-G0
C 14	84.6	4.1	1242	10	CL068807	CL068807	CH216-115
C 15	84.6	4.1	2270	10	AG279272	AG279272	Mus muscu
C 16	81.4	3.9	994	11	CNS04NOJ	AL298972	Tetraodon
C 17	81	3.9	1372	1	AJ327522	AJ327522	AJ327522
C 18	80.6	3.9	1371	10	CG748753	CG748753	P042-4-A0
C 19	79.8	3.8	1038	11	CNS0617M	AL403832	T3 end of
C 20	79.8	3.8	1101	10	CNS0039G	AL063921	Drosophi
C 21	79.8	3.8	1238	1	AJ325855	AJ325855	AJ325855
C 22	79.4	3.8	1254	10	AG349719	AG349719	Mus muscu

ORIGIN		BAC library"	
Query Match		4.6%; Score 95.2; DB 10; Length 1981;	
Best Local Similarity		43.2%; Pred. No. 1.9e-07;	
Matches 620; Conservative		0; Mismatches 798; Indels 16; Gaps 3;	
QY	658	AAAGAAATATACCTTAAATAGTAACTATGTGCGAAATACCTATAGAGAGGACTAAAT	717
DB	1978	AAATAAAAAACAGTATATAAATAAAAAAATAAATAAAAAAATAAGAAATAAATAA	1919
QY	718	AACTTCGAAACCACTTAATAGATGGAGTATATTTAATCATTTATCGAAGATATG	777
DB	1918	AAAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1859
QY	778	ACTATTACTGTATTAGATACCTACGCTCAATTTCTTTT-----TGATATAA	826
DB	1858	TAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1799
QY	827	AGAGATACAAAGATTCAATAGGAAGATAGGTGGCAATTAAACTGAACCTTACAAGAAA	886
DB	1798	ATATATAAAAAATAAATAACACAAAAAATAAATAAATAAATAAATAAATAAATAA	1739
QY	887	TTTATACACTGAATAAATTTTGACCGCTTACTTTACCTTGAATTCACCCCAATCTCG	946
DB	1738	TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1679
QY	947	CTATAATGGAATAAATTTAAACACGTTTCAGGGCTTAGATTATTTTCATTTTAGATGAAC	1006
DB	1678	AAAAATCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1619
QY	1007	TTATATTTTATACAAAAATGAACGTACGGGAATCGTTTAGTTGGTATTTGCGAATCGTA	1066
DB	1618	ATAAATATCAATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1559
QY	1067	ATAGATCTACTTGTACGACAGGAAGTGAATATATATGAGAGAAAGACAGGCTCCAC	1126
DB	1558	AAATAATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1499
QY	1127	CCACAAACAAACCTTTAATACCAATTTGAACTTCAATTTGTAACCTGTAGAC	1186
DB	1498	ATCAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1439
QY	1187	AGTAATCTCTACTTCCCTTTTCTTAAACATATATCTTCAATATCAATCAAAATGAACTTT	1246
DB	1438	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1379
QY	1247	ATTTAATATTTCACTAGTAAATAATTAACATATTCAGCTGGGGGAATTTATCTAATG	1306
DB	1378	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1319
QY	1307	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1366
DB	1318	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1259
QY	1367	CAAAATGTTTACCAAGCTATAATAGTTATAGTCATATTTTATCCCAAGTTTCTTTATTTA	1426
DB	1258	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1199
QY	1427	ATTATTCTTATAAATTTAGCTTACCTGAATATATATATACAGTGGCAATAGGATGA	1486
DB	1198	AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1139
QY	1487	CACACAGTAGTGT-----ATAGAAATAATGCAATATCAGATAAATAAATAATCAATGATCC	1543
DB	1138	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1079
QY	1544	CAGCAATCAAGGTACAGCTTTGTGATACAACTCTTAAGGTAAATTGAAGGACCTGGTCATA	1603
DB	1078	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1019
QY	1604	CAGGAGAACTTGGTTTATTTTACAAAGTCAGGGCGTTTAGAGATTACATGTAGAACCTC	1663
DB	1018	AAAAAAAAAATACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	959
QY	1664	CTAATTTTACACAATCTTTATTATCATTTAGACTTCGTGATACCGTACAAATGGTCTGGAAATA	1723
DB	958	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	899
QY	1724	CTCTTCTTAATATCTCTTTACAATACCAGGAGTATATGAATACCACTTCAACGACTCA	1783
DB	898	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	841
QY	1784	ACAACACTTTTTCTGTGATCAAAATTATAATAATTTACAATACGAGATTTTGGGTATTTC	1843
DB	840	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	781
QY	1844	AATTTCCAAGTACAGTAACATTTACCTTTAAATCGAAACATACCATTTATTTAATCGTG	1903
DB	780	ATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	721
QY	1904	CAGATGTATCAATTTCAATTTTAAATCATTTGATTAATTTCAATTTTACCAATTTACTTCT	1963
DB	720	ATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	661
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ACCESSION			
CG757503			
VERSION			
CG757503.1 GI:37986131			
KEYWORDS			
GSS.			
SOURCE			
Pristionchus pacificus			
ORGANISM			
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;			
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REFERENCE			
1 (bases 1 to 1392)			
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,			
Buntjer,J., van der Meulen,M. and Sommer,R.J.			
An integrated physical and genetic map of the nematode Pristionchus			
pacificus			
Mol. Genet. Genomics 269 (5), 715-722 (2003)			
JOURNAL			
PUBMED			
12884007			
COMMENT			
Contact: Sommer RJ			
Evolutionary Biology			
Max-Planck-Institute for Developmental Biology			
Spemannstr. 37-39, Tuebingen D-72076, Germany			
Tel: 00497071601371			
Fax: 00497071601498			
Email: ralf.sommer@tuebingen.mpg.de			
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P048-1-C01.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
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CG753083
CG753083.1 GI:37977199
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Pristionchus pacificus
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1896)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
12884007
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

Location/Qualifiers
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source

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LOCUS   CL118721
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ACCESSION
CL118721
VERSION
CL118721.1 GI:40612356
KEYWORDS
Xenopus tropicalis
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE
1 (bases 1 to 1608)
Mardis, E. and Wilson, R.
Kremitski, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
A physical map of the xenopus tropicalis genome
Unpublished (2003)
TITLE
A physical map of the xenopus tropicalis genome
JOURNAL
Unpublished (2003)
COMMENT
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 75000 Std Error: 0.00
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RESULT 9

AG350139/c

LOCUS

DEFINITION AG350139 1489 bp DNA linear GSS 18-DEC-2004

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ACCESSION AG350139

VERSION AG350139.1 GI:47923449

KEYWORDS GSS.

SOURCE Mus musculus molossinus (Japanese wild mouse)

ORGANISM Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and Shiroishi, T.

Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis

Genome Res. 14 (12), 2439-2447 (2004)

15574823

2 (bases 1 to 1489)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp)

Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyada, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: abe@rtc.riken.jp

PRIMERS

Sequencing : TJ

LIBRARY

Vector : pBACe3.6

R Site 1 : EcoRI

R Site 2 : EcoRI

FEATURES

source

1..1489

Location/Qualifiers

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ORIGIN

Query Match 4.2%; Score 88.4; DB 10; Length 1489;

Best Local Similarity 43.4%; Pred. No. 3.5e-06;

Matches 605; Conservative 0; Mismatches 763; Indels 20; Gaps 4

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Db      1307  AATATATAATPAGAAATTAATATATATAGTANAATTTTAAATTAATAATATAATATATATT 1248
Qy      894  AACTGAATTAATTTTGGACCGTCTTACTTTACCTTGAATTTCAACCCCAATCTCGCTATAAT 953
Db      1247  TTTAGATTTANAATTAGTAATTTATTTATTAATTTTATAATAATTTTNAATTTAATAAATAAT 1188
Qy      954  GGAATATAATTTAAACAGGTTTCAGGGCTTAGATTAATTTTCATTTTGTAGAGAACTTATATT 1013
Db      1187  AATTAATATAATATATAAATTTATATTAGTAATTTATATATATATATATAATAATATAATA 1128
Qy      1014  TTATACAAAATAAGAAACGTACGGGAATCGTTTGTGTTGCGAATCGTAATAGATC 1073
Db      1127  TAATTATATAATTAATATAAATAAATAATTAATTAATTAATAAAGTTTATATATT 1068
Qy      1074  TACTTATGCTACGACGGAACCTGAAATTTATATATGGAAGAAGAACAGGTCACCCACAAC 1133
Db      1067  AAATAATATATTATATATGAATAAATAATATAATTAATTAATAAAGATTTTAATTTATT 1008
Qy      1134  AAAAACTTTAATACCAATTTGAATCCCTATAAAGTTTCAATTTGTAACGTAGACAGAATAAC 1193
Db      1007  AATTTTAATAAGANTAATAATAATATATATATAATAAATAAGTAAAT-ATATATAAATTTAT 949
Qy      1194  TCCTACTTCCCTTTTCCCTAACATATACTTTACAAATTAATCAAAATTTGAACCTTTATTAA 1253
Db      948  ATAAATTAATAATATAAATAAATAATTTTAAATTTTATAAATAATTAATTAATAAATAAT 889
Qy      1254  TAATTCACCTAGTAATAAATTAACATATTCAGCTGGGGGAATTTATCTAATGATAAAAA 1313
Db      888  ATATTATATAAATTTATATATTTATATTAATAAATAAATAAATAATATATAGATAAATA 829
Qy      1314  ACAACTGATTTTCAATTTCTCTGTAATAAAGAACTGTAACCAATTTATTAATCCAATTTG 1373
Db      828  TATAATTATAAATAATTTATATATATAATTAAATAATAATAATATATATATATATTTT 769
Qy      1374  TTTACCAAGCTATAAGTATATAGTCATATTTTATCCAGTTTCTTTTATTAAATTATTC 1433
Db      768  TTAATTTAATTAATAATAATTAATAATTAATAATTAATAATTAATAATTAATAATATAT 709
Qy      1434  CTATAAAATTTGGATTAGCGCTAAATATATATATACAGGTGCAATAGGATGGACACACAG 1493
Db      708  ATATAAATTTAAATAATTTATTAATAAATTTTAAATAATATTAT----- 665
Qy      1494  TAGTGTTAATAGAAAATAAGCAATATCAGATAAATAATTAACAATGATCCAGCAATCAA 1553
Db      664  TAATTTAAATATATATAAATAATAAATAATTTATTTATAATAATAATAATTAATTTAATA 605
Qy      1554  AGGTACAGCTTTGATACAAACCTCAAGGTAATTTGAAGGACCTGGTCATACAGAGGAAA 1613
Db      604  TAATTATATTATTTTAAATAATAATAATATTTAATAATATAATAAATAATAAATTTTAT 545
Qy      1614  CTTGGTTTATTTACAAAGTCAAGGGCGTTTAGAGATTACATGTAGAACTCTCAATTTCTAC 1673
Db      544  ATATATATAAATATATTATTTTAAATTTTAAATAATTTATTTAATTTATTAATAATAT 485
Qy      1674  ACAATCTTATACATTTAGACTTCGATACGCTACAAATGGTGGGAAATACTCTTCTCTAA 1733
Db      484  AATATTATTAATTAATTTAAATTTGAATATTTAATAATAATAATAATAATAATTTTAAATTA 425
Qy      1734  TATATCTCTTACATAACACGAGGTAATAGGAATPACCACTCAACGACTCAACAAACACTTT 1793
Db      424  TATATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 365
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Qy      1794  TTCTGTGTCACAAATTAATAATAATTTACAATPACGAGAGATTTTGGGTATTTTCCAATTTCCAAG 1853
Db      364  TTTTATAATAATAATAATAATAAATAAATTTTATAAATAATTTTAAATTTTATTTAATATATAT 305
Qy      1854  TACAGTAACATTACCTTTTAAATCGAAACATACCATTTATATTTAAATCGTGACATGTATC 1913
Db      304  AATATAATTTATTATATTTAAATTTATTTTAAATTTTAAATTTTAAATTTTAAATTTAATAAT 245
Qy      1914  AAATTCAAATTTTAAATCATTGATAAAAATTTGAAT-TTATACCAATTTACTTCTCTGTAGGCC 1972
Db      244  ATATAAATAATTTTATTTTAAATTTTAAATAAATAATTTTATATATAAATTTTATATATAAT 185
Qy      1973  AAAATAGAGAAAACAAAATTTAGAACTATCCAAACAAAATAAATAATATATATTTTCCAAA 2032
Db      184  TTATTTTAAATAATTTTATTTAAATTAATTTTAAATAATTTATAAATAATATATACACACAGGTG 125
Qy      2033  ATCATACAAAATAAT 2046
Db      124  GTCACACATATTT 111

RESULT 10
CNS010MP      734 bp      DNA      linear      GSS 26-JUL-1999
LOCUS      Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION      BACN04L20 of DrosBAC library from Drosophila melanogaster (fruit
      fly), genomic survey sequence.
ACCESSION      AL0099163
VERSION      AL0099163.1 GI:5610774
KEYWORDS      GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM      Drosophila melanogaster
      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
      Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 734)
AUTHORS      Genoscope.
TITLE      Direct Submission
JOURNAL      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
      BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
      - Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
      collaboration with the European Drosophila Genome Project (EDGP) -
      http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
      library (Dros BAC) was made by Alain Billaud at CEPH (Centre
      d'Etude du Polymorphisme Humain) with funding provided by a MRC
      project grant. The DNA was prepared from embryos by Alain Bucheton
      and Genevieve Payan. It has been constructed in the vector
      pBelobAC11.

FEATURES
      source
      1..734
      /organism="Drosophila melanogaster"
      /mol_type="genomic DNA"
      /db_xref="taxon:7227"
      /clone="BACN04L20"
      /clone_lib="DrosBAC"
      /plasmid="pBelobAC11"
      /note="end : T7"

ORIGIN
      Query Match      4.2%; Score 87.2; DB 10; Length 734;
      Best Local Similarity 34.9%; Pred. No. 5.9e-06;
      Matches 248; Conservative 111; Mismatches 341; Indels 10; Gaps 1;

Qy      1250  TAAATAATTTCACTAGTATAATAATTAAACATATTTAGCTGGGGGAATTTATCTTAATGATA 1309
Db      9      TACANTACTCAWATATNNMACWTAATAAATTTATAAAAAAATAATATTATATATTTA 68
Qy      1310  AAAAAACAACTGATTTTCAATTTCTGTAAAAAAGACTGTAAACCAATTTATTAATCCAA 1369
Db      69  TATAWAATWTATAAAAAAAMWTTTCAAAATTTTMAAAAAAAMWAAWWTAMHMAWAATTTWA 128
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Db      435 AAAAAATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATAATATATAATTTTAA 376
Qy      1914 AAATTCATTTTAAATCGATGATTAATGAATTTATACCAATTAATCTCTCTGAGCCCA 1973
Db      375 AAAAAAAAAAATAAAAAAAAAAATAAAAAAAAAAATAAAAAAAAAAATAATTAATTTATA 316
Qy      1974 AAATAGAGAAAAACAATAATAGAACTATCCAAACAAATAAATAATATATTTTCAAA 2033
Db      315 AATAAAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 256
Qy      2034 TCATACAAAAATACCTTTAAATATAGAGCCACAAACTATGATATTGATT 2083
Db      255 TTTATAAAAAATATAAANAANAANAANAATTTAATAATAAATAAT 206

RESULT 12
CNS00EVL
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence 17 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL069706
VERSION
AL069706.1 GI:4949849
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
REFERENCE
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamooser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
FEATURES
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            /mol_type="genomic DNA"
            /db_xref="taxon:7227"
            /clone="BACR29B23"
            /note="end : T7"

ORIGIN
Query Match          4.1%; Score 86; DB 10; Length 1101;
Best Local Similarity 34.5%; Pred. No. 9.9e-06;
Matches 220; Conservative 106; Mismatches 311; Indels 1; Gaps 1;

Qy      875 TTACAAGAGAAATTTATACAACATGAATTAATTTTCACCGCTCTTACTTACCTTGAAATTC 934
Db      463 TTTTMMWWWWAATTTTWWAAAWAAATTTATWAATWAAAWAAWWAATTTTWWWWTAAAT 522
Qy      935 AACCCAAATCTCGCTATAATAGGAATATAATTTAAACGTTTCAGGGCTTAGATATTTTCAT 994
Db      523 WTTTAAWTTTAAWTTAAWAAAAAAWATAATTTTAAWAAATATAWAAATTAWAAWTTA 582
Qy      995 TTTTAGATGACTTATATTTTATACAAATAAATAAGAAACGTACGGGAATCGTTAGTTGTA 1054

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Db      583 TATTATATTAATAATTTATTAATAAATAAATAATTTTWTATAAATAATTTTAAATAAT 642
Qy      1055 TTGCGAATCGTAAATAGATCTACTTATGCTACACAGGAACCTGAAATATATATATGAGAAA 1114
Db      643 TAAATTAATTTATTAATAATTAATTTTAAATAATTTTAAATAATTTTAAATAAATAAATAA 702
Qy      1115 GAACAGGTCACCCCAACAACAATACTTTTAATACCATTTGAAATCCTATAA-AGTTTCAAT 1173
Db      703 AAATATWAAATAATTAATAAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAA 762
Qy      1174 GTAACCTGATAGACAAGTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1233
Db      763 TATATTTTAAATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 822
Qy      1234 CAAATTTGAATTTTATTAATAATTTCACTAGTAATAATAATAATAATAATAATAATAATAATA 1293
Db      823 WAAWATAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 882
Qy      1294 AATTTATCTAATGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1353
Db      883 AWTTTTAAATAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 942
Qy      1354 CCAATTTATTAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1413
Db      943 ATTATTTTAAATAATTTTAAATAATTTTAAATAATTTTAAATAATTTTAAATAATTTTAA 1002
Qy      1414 TTTTCTTTTATTAATTTTCTTATTAATAATAATAATAATAATAATAATAATAATAATAATAA 1473
Db      1003 ATATATTTTAAATAATTTTAAATAATAATAATAATAATAATAATAATAATAATAATAA 1062
Qy      1474 GCATTTAGATGACACACAGTAGTGTGTTAATAGAAATAA 1511
Db      1063 AWTATATATTTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 1100

RESULT 13
CG754863/c
LOCUS
DEFINITION
P050-2-G05.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
ACCESSION
CG754863
VERSION
CG754863.1 GI:37980782
KEYWORDS
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 1391)
AUTHORS
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE
An integrated physical and genetic map of the nematode Pristionchus
pacificus
JOURNAL
Mol. Genet. Genomics 269 (5), 715-722 (2003)
PUBMED
12884007
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
FEATURES
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        1..1391
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            /mol_type="genomic DNA"
            /strain="California"
            /db_xref="taxon:54126"
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            /note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

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RESULT 14	CL068907/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source	ORIGIN
	CL068907	1242 bp	DNA linear	GSS 31-DEC-2003												
	CH216-115B3_Sp6.1	CH216	Xenopus tropicalis genomic clone													
	CH216-115B3	genomic survey sequence.														
	CL068907															
	CL068907.1	GI:40524720														
	GSS.															
	Xenopus tropicalis	(western clawed frog)														
	Xenopus tropicalis															
	Eukaryota; Metazoa;															
	Amphibia; Batrachia;															
	Xenopodinae; Xenopus;															
	1 (bases 1 to 1242)															
	Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,															
	Mardis, E. and Wilson, R.															
	A physical map of the xenopus tropicalis genome															
	Unpublished (2003)															
	Contact: Richard K Wilson															
	Genome Sequencing Center															
	Washington University School of Medicine															
	Email: submissions@wustl.edu															
	Insert Length: 175000	Std Error: 0.00														
	Seq primer: Sp6 ATTTAGTGACACTATAG															
	Class: BAC ends															
	High quality sequence start: 7															
	High quality sequence stop: 57.															
	Location/Qualifiers															
	1. 1242															
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	/strain="Nigerian frog"															
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	/clone="CH216-115B3"															
	/sex="male"															
	/cell_line="Stock 248 F7A2, inbred N7"															
	/clone_lib="CH216"															
	/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis															
	BAC library"															
	Query Match	4.1%	Score 84.6;	DB 10;	Length 1242;											
	Best Local Similarity	45.2%;	Pred. No. 1.8e-05;													
	Matches	421;	Conservative	0;	Mismatches 506;	Indels	4;	Gaps	3							
Qy	538	AAATTTTCATTTAAATTTATTACACAAAGGTGCTGCAATTTGGCTGATGAATGGAATGCAGAT	597													
Db	947	AAATATTAAATTAATTAATAATAAATAAATAATAATAATAATAATAATAATAATAATAATAATA	888													
Qy	598	ATACATCCTTCACAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATTAACCTTTTA	657													
Db	887	ATAATTATAATAAAAAAATTAATAATAAAAAATTAATAATAAAAAATTAATAATAATAATAATA	828													
Qy	658	AAAGAAATATACCTAAATATAGTAACCTATTGTGCAATACTATAGAGAGGACTAAAT														

Db	587	ATATAATAAAAAATTATTATTAAATAATATTAAATTTATAAAATTTATAATATATATATAATAA	528
Qy	958	TATAATTTAACACGTTTCAGGGCTTAGAATTAATTTTCATTTTTTTAGATGAACCTTATATTTTAT	1017
Db	527	TATTATTATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	468
Qy	1018	ACAAAAATGAACGTCACGGAAATCGTTTAGTTGGTATTCGGAATCGTAATAGATCTACT	1077
Db	467	AAAAAAATTTAAAAAAGAAATTT	408
Qy	1078	TATGCTACGACAGAACTGAAT-TATATATGAGAAAGAACACAGGTCACCCACACAAA	1136
Db	407	TATTTTAATATTATAAAAAAATAATATATTAATTAATTAATAAAAAAATAATAATA	348
Qy	1137	AACCTTTAATACCAATTTGAATCCATATAAAGTTTCAATTTGTAATCTGATGACAACTCTC	1196
Db	347	ATAAATTAATAATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	288
Qy	1197	TACTTCCCTTTTCCTTAACATATACCTTTACAATTAATCAAAATGAACCTTTTATAATAA	1256
Db	287	TAAATATAATAACAATAAAAAATA--TAAAAATAAATTAATAATTAATAATAATA	230
Qy	1257	TTCACTAGTAATAAATAACATATTTCAGCTGGGGAAATTTATCTAATGATATAAAAAAC	1316
Db	229	AT-ATATAAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	171
Qy	1317	AACGTGATTTTCAATTTCTGTAAAAAAGACTGTAAACCAATTAATTAATCCAAATTTGTT	1376
Db	170	TTAAATATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	111
Qy	1377	ACCAAGCTATAATAGTTATAGTCATATTTATCCAGATTTCTTTTATTTAAATTTCCCTA	1436
Db	110	CTTTTTTTTTTTCTTTCTTTTATTTTGTGGCTGGCTCCCGCCNCCCTATTATATA	51
Qy	1437	TAAATTTGGAATTAGCGCTAAATATATATAT 1467	
Db	50	AAAAAATAGTATCATCCTTAATAATTTATGT 20	
RESULT 15			
AG279272/c		2270 bp DNA linear GSS 18-DEC-2004	
LOCUS		Mus musculus molossinus DNA, clone:MSMg01-050A24.TJ, genomic survey	
DEFINITION		sequence.	
ACCESSION		AG279272	
VERSION		AG279272.1	
KEYWORDS		GI:47852149	
SOURCE		GSS.	
ORGANISM		Mus musculus molossinus (Japanese wild mouse)	
REFERENCE			
AUTHORS		Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and Shiroishi, T.	
TITLE		Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis	
JOURNAL		Genome Res. 14 (12), 2439-2447 (2004)	
PUBMED		15574823	
REFERENCE		2 (bases 1 to 2270)	
AUTHORS		Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.	
TITLE		Direct Submission	
JOURNAL		Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)	
COMMENT		Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute Bio Resource Center. The Institute of Physical and Chemical Research (RIKEN) 3-1-1	

		Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp PRIMERS Sequencing : TJ LIBRARY Vector : pBACe3.6 R.Site 1 : EcoRI. R.Site 2 : EcoRI. Location/Qualifiers 1. .2270 /organism="Mus musculus molossinus" /sub_type="genomic DNA" /sub_species="molossinus" /db_xref="taxon:57486" /clone="MSMg01-050A24.TJ" /sex="male" /tissue type="mixture of kidney and spleen" /clone_lib="MSMg01 Mouse Male BAC Library"	
FEATURES			
source			
Query Match	4.1%;	Score 84.6;	DB 10; Length 2270;
Best Local Similarity	42.7%;	Pred. No. 1.8e-05;	
Matches	650;	Conservative	0; Mismatches 869; Indels 5; Gaps 4;
Qy	549	AAATTTATTACAAACGAGTGGCTGAATTCGCTGATGAATGGAATGCAGATATACATCCTTC	608
Db	1971	AAACATTTAATATATAAATAGATAGATAAAAAATGAATATAAAGAAATATTAGTATAATA	1912
Qy	609	ACAAATTGGAACCTAATGCTGGAAACATCAGATGACATTTATAAACTTTTAAAAAGAAATAT	668
Db	1911	ATAAAAAAGTAACCTAATAAGAAAAAGAAAAAATAAATAAATAAATAAATAAATAA	1852
Qy	669	ACCTAAATATAGTAACCTATTTGCAAAATACCTATAGAGAAGGACTAAATAAACTTCGAA	728
Db	1851	TGAATAAATAAAAAAATAAATAAAGATAGATAAATAATAAGAAAAATAAATAATAAAT	1792
Qy	729	CGAACCTAATAGAGATGGAGTATTTTAATGATTTATCGAAGATATATGACTATTACTGT	788
Db	1791	AAATTAATAAAGAAAAAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATA	1732
Qy	789	ATTAGATACATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATTTCAATAGG	848
Db	1731	ATATAAATAAGTTAGAAATAAAGTAATAAATAAATAAATAAATAAATAAATAAATAA	1672
Qy	849	AAGAATAGGTGGCATTAACAACTGAACTTACAAGAGAAATTTATACAACTGAATAATTT	908
Db	1671	ATAAAAATTAAAAACATAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	1612
Qy	909	TGACCGCTCTTACTTACCTTGAATTTCAACCCCAATCTCGCTATAATGGAATATAATTTA	968
Db	1611	AAAAAANAAGATAAAGATAAAGAAAAA--AAGAAAAATATATAAATAAATAAATAAATA	1553
Qy	969	ACGTTTCAGGCTTAGATTAATTTTTCATTTTTCATGAACTTTATATTTTATACAAAAATGA	1028
Db	1552	ATATATAATAATAAATAAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	1493
Qy	1029	AACGTAACGGAAATCGTTTAGTTGGTATTCGGAATCGTAATAGATCTACTTTATGCTAG	1088
Db	1492	TATAATAATAATTAATAAAGAAAAAATAAATAAAGAAAAAATAAATAAATAAATAAATA	1433
Qy	1089	AGGAAT--GAATTTATATATGAGAGAAAGAACAGGTCACCCACACAAAAAATTTAATA	1146
Db	1432	AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1373
Qy	1147	CAATTGGAATCCTATAAAGTTTCAATTTGTAACCTGATAGACAGTAACCTCTACTTCCCCT	1206
Db	1372	AAATTAATGAATAATAATAACATAAAGAAATAAAGAAATTAATAAATAAATAAATAAATA	1313
Qy	1207	TTTCCTAACATATACCTTTACAATTAATCAAAATGGAATTTTATTTTAATAATTTACCTAGT	1266
Db	1312	TTTATNTATAGATAAATAAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	1253

Search completed: February 15, 2006, 02:57:59
Job time : 8397 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	331.4	15.9	3543	3	US-09-224-024-27	Sequence 27, Appl
2	331.4	15.9	3543	6	PCT-US94-07902-27	Sequence 27, Appl
3	158	7.6	2061	3	US-09-224-024-30	Sequence 30, Appl
4	158	7.6	2061	6	PCT-US94-07902-30	Sequence 30, Appl
5	92.6	4.4	3507	2	US-08-315-468-3	Sequence 3, Appl
6	79.6	3.8	3444	2	US-08-349-867-22	Sequence 22, Appl
7	79.6	3.8	3444	2	US-08-349-867-26	Sequence 26, Appl
8	79.6	3.8	3444	2	US-08-239-476-22	Sequence 22, Appl
9	79.6	3.8	3444	2	US-08-239-476-26	Sequence 26, Appl
10	79.6	3.8	3444	2	US-08-598-305A-22	Sequence 22, Appl
11	79.6	3.8	3444	2	US-08-598-305A-26	Sequence 26, Appl
12	79.6	3.8	3444	2	US-08-639-923A-22	Sequence 22, Appl
13	79.6	3.8	3444	2	US-08-639-923A-26	Sequence 26, Appl
14	79.6	3.8	3444	6	PCT-US95-05431-22	Sequence 22, Appl
15	79.6	3.8	3444	6	PCT-US95-05431-26	Sequence 26, Appl
16	79.6	3.8	3450	2	US-08-349-867-20	Sequence 20, Appl
17	79.6	3.8	3450	2	US-08-239-476-20	Sequence 20, Appl
18	79.6	3.8	3450	2	US-08-598-305A-20	Sequence 20, Appl
19	79.6	3.8	3450	2	US-08-639-923A-20	Sequence 20, Appl
20	79.6	3.8	3450	6	PCT-US95-05431-20	Sequence 20, Appl
21	79.6	3.8	3522	2	US-07-828-788A-9	Sequence 9, Appl
22	79.6	3.8	3522	2	US-08-349-867-24	Sequence 24, Appl
23	79.6	3.8	3522	2	US-08-349-867-28	Sequence 28, Appl
24	79.6	3.8	3522	2	US-08-239-476-24	Sequence 24, Appl

Matches 856; Conservative 0; Mismatches 697; Indels 38; Gaps 7;

QY 499 TATATAACGCTATTAATCTACTACCTATTTATGCGCAAGCTGCTAAATTTTCAATTTTAAATTTATTA 558
DB 604 TATAACATCTAGTATTAATCTAGTTATGCAACAGCAGCAACCTTACATCTGACTGTATTA 663
QY 559 CAACAAGGTGCTGAATTTGGCTGATGAATGGAATGCGAGATATACATCCCTTCACAATTTGAA 618
DB 664 AATCAAGCCGCTCAAAATTTGAAGGCTATTTTAAAAACAATCGACAAATTCGATTTATTTAGAG 723
QY 619 CCTAATGCTGGAACATCAGATGACTATTAATACTTTTAAAAAGAAATATACCTTAATAT 678
DB 724 CCTTTGCC---AACAGCAATGATTAATTTTCCAGTATTTGACTTAAGCTATAGAAGATTAC 780
QY 679 AGTAACCTATTGTGCAAAATCTATAGAGAGGACTAAATAAACTTCGAAACGAACTTAAT 738
DB 781 ACTAATATTGTGTAACTTATATAAAAGGATTAATTTTAAATTAACGACGCGCTGAT 840
QY 739 ATGAGATGGAGTATATTAATGATTTATCGAAGATATATGACTATTACTGTATTAGATATCT 798
DB 841 AGTAATCTTGTATGGAATATAAACTCGGAACACATACAATACGTATCGAAACAAAATGACT 900
QY 799 ATCGCTCAATTTTCTTTTATGATATAAGAGATACAAGATTCAAATAGGAAGATAGT 858
DB 901 ACTGCTGTATTAGATCTTGTGCACTCTTTCCTAATTTATGATGATGATGATGATGATGATGAT 960
QY 859 GGCATTTAAACCTGAACCTTCAAGAGAAATTTTATCAACTGAAATAAAATTTTGACCGCTCTT 918
DB 961 GGTGCTCAATCTGAACCTTACTCGAGAAATTTAT------CAGGTACTTTAACTTCGAAGA 1013
QY 919 ACTTACCTTGAATTCGAACCAATCTCGGTATTAATGGAATATTAATTTTAACACGCTTCAGGG 978
DB 1014 AAGCCCTTATAATATTATGACTTTCAATATCAAGAGGATTCACCTTACACGTAGACCGCA 1073
QY 979 CTTAGATTAATTTTCAATTTTATGATGAATTTATATTTTATACAAAATGAAACGTACGGG 1038
DB 1074 TTTATTACTTGGCTGATCTTTGAAATTTTATGAAAGCGCAAACTACTCTCTTAATA 1133
QY 1039 AATCGTTTATGTTGGTATTCGGAATCGTAATAGATCTACTT-ATGCTACGACAGGAACCTGA 1097
DB 1134 TTTTTCACCGCATTAATAATGTTTCAATACACATCTGATTAATATATATCCCAAAATC 1193
QY 1098 AATTATATATGGAAGAAGAACAGGTCACCCCAACAACAAATCTTTAATACCATTTGAATC 1157
DB 1194 TAGTGTTTTGGAAATCACAATGTAACTGATAAATTAATAATCTCTTTGGTTTGGCAACAAA 1253
QY 1158 CTATAAGTTTCAATTTGTAAGTACTAGACAGAACTCTACTTCCCTTTTCCCTAACAT 1217
DB 1254 TATTTATATTTTATTAATGCTAAGCTTAGATTAATAATATCTTAATGATTTATA 1313
QY 1218 ATACTTTTACAATTAATCAATTTGAATCTTTTATTAATAATTCACCTAGTAATAAATTAAC 1277
DB 1314 TAATATTAGTAAATGGAATTTTATATACTAATGTTACTAGACTTTTGGAGAAAGAACT 1373
QY 1278 ATATTACGCTGGGGGAATTTATCTAATGATAAAAAACAACGTATTTCAATTTCTCTGT 1337
DB 1374 TACAGCAGGATCTGGGCAAAATTAATCTATGATGTAATAAATAATTTTTCGGGTACCAAT 1433
QY 1338 AAAAAAGACTGTAACCAATTAATTAATCCAATTTTACCAAGCTATAATAGTTATAG 1397
DB 1434 TCTTAAACGAGAGAAATCAAGCAATCCCTACCCCTTTTCCAAATATGATTAATAG 1493
QY 1398 TCATATTTTATCCAGTTTCTTTTATTAATTTATTTCTATAAATTTGGATTAGCGCTAAA 1457
DB 1494 TCATATTTTATCATTTTATTAAGAGTCTTAGTATCCC-----TGCAACATA 1538
QY 1458 TATATTATATACAGGTGCAATTAGATGGACACACAGTAGTGTTAATAGAAAATATGCAAT 1517
DB 1539 TAAACTCAAGTGATACGTTTCTTTGGACACACTCTAGTTGTTGATCTCTTAAAAATACAAT 1598
QY 1518 ATCAGATAAAATTAATTAACATGATCCAGCAATCAAGGTAAACAGTCTTGATCAAACTC 1577
DB 1599 TTATACACATTTAACTACCAAAATTCAGCTGTAAAAAGCGAATTCACCTTGGGACTGCTTC 1658

QY 1578 TAAAGTAATTGAAGGACCTGGTCATACAGGAGAAACTTTGGTTTATTTTACAAGTCAAGG 1637
DB 1659 TAAAGTTGTTTCAAGGACCTGGTCATACAGGAGGGGATTTAAATTTGATTTTCAAGATCA--- 1715
QY 1638 GGGTTTAGAGATTACATAGAACTCCTAAATCTACACAACTCTTATTAATTAATAGACTTCG 1697
DB 1716 ---TTTCAAAATTAATCATGTCAACCTCAAAATTTTCAACAACTCGTATTTTATAGAAATTCG 1772
QY 1698 ATACGCTCAAAATGGTGGTGGAAATCTCTTCTTAATATATCTCTTACAAATACCAGAGT 1757
DB 1773 TTATGCTTCAATGGAGCGCAATACAGGACTGTATAAATCTTAGTATCCAGGG- 1831
QY 1758 AATAGAAATACCACTCAACGACTCAACAACTCTTTTCTGGTACAAATTAATTAATTT 1817
DB 1832 --TAGCAGAACTGGGTATGGCACTCAACCCCACTTTTCTGGTACAGATTTATACGAATTT 1889
QY 1818 ACAATACGAGATTTTGGGTATTTCCAAATTTCCAAAGTACAGTAACTTACCTTTTAATCG 1877
DB 1890 AAAATATAAGATTTTTCAGTACTTGAATTTTCTAACGAGGTGAATTTTGTCTCCAATCA 1949
QY 1878 AAACATACCATTTTATTTAATTCGTGCGAGATGTAT---CAAAATTCAAATTTTAAATCA 1934
DB 1950 AAACATATCTCTGTTGTTTAACTCGTTCGATGTATATACAAACACACAGTACTTTATGA 2009
QY 1935 TAAATTTGAATTTATACCAATTTACTTCTCTGTCGCCAAATAGAGAAAAACAAAAAT 1994
DB 2010 TAAATTTGAATTTTCTGCAATTTACTCGTTCTTATAAGAGAGGATAGAGAGAAAAACAAAAAT 2069
QY 1995 AGAACTATCCAAACAAATAAATAATACATTTTTCACAAATCATACAAAAATCTTTTAA 2054
DB 2070 AGAAACAGTACAAACAAATAAATAATTAATACATTTTATGCAAACTCTATAAAAAACACTTTACA 2129
QY 2055 TATGAAGCCACAAACTATGATATTGAATTA 2085
DB 2130 ATCAGAACTTACAGATTATGACATAGATCA 2160

RESULT 2

PCT-US94-07902-27

; Sequence 27, Application PC/TUS9407902

; GENERAL INFORMATION:

; APPLICANT:

; APPLICANT: Street address: 4980 Carroll Canyon Road

; APPLICANT: City: San Diego

; APPLICANT: State/Province: California

; APPLICANT: Country: US

; APPLICANT: Postal code/Zip: 92121

; APPLICANT: Phone number: (619) 453-8030

Fax number: . (619) 453-6991

; APPLICANT: Telex number:

; TITLE OF INVENTION: Materials and Methods for the Control of

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/07902

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Saliwanchik, David R.

; REGISTRATION NUMBER: 31,794

; REFERENCE/DOCKET NUMBER: MA79

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3543 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-07902-27

Query Match 15.98; Score 331.4; DB 6; Length 3543;

Best Local Similarity 53.8; Pred. No. 3.3e-56;

Matches 856; Conservative 0; Mismatches 697; Indels 38; Gaps 7;

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QY 499 TATAAAACGCTATTACTACCTATTATGTCGCAAGCTGCTAAATTTTCAATTTTAAATTTATTA 558
DB 604 TATAACATACATAGTATTATCTAGTTATGCAACAGCAGCAAACTTACATCTGACTGTATTA 663
QY 559 CAACAAGGTGCTGAATTTGGCTGATGAATGGAAATGCAGATATACATCTTCCAAATTTGAA 618
DB 664 AATCAAGCGCTCAAAATTTGAAGCGTATTTAAAAACAATCGACAATTCGATTTATTAGAG 723
QY 619 CCTAATGCTGCAACATCAGATGACTATTATAAATCTTTTAAAGAAATATATACCTAAATAT 678
DB 724 CCTTTGCC---ACAGCAATTTGATTTATCCAGTATTGCTAAAGCTATAGAAGATTAC 780
QY 679 AGTAACCTATTGTGCAATACCTATAGAGAAGGACTAAATAAATCTTGAAGAAACGAACTTAAT 738
DB 781 ACTAATTTATTTGTGTAACAATTTATAAAGGATTAATTTAATTAACAACGACCTGAT 840
QY 739 ATGAGATGGAGTATATTAATGATATATCGAAGATATATGACTATTACTGTATTAGACT 798
DB 841 AGTAATCTTGATGAAATATAAATCGGAACACATACATACGATTCGAAACAAAAATGACT 900
QY 799 ATCCCTCAATTTCTTTTATGATATAAGAGATACAAGATTCATATAGGAAGAAATAGGT 858
DB 901 ACTGCTGTATTAGATCTTTGTCGACTCTTCTCCTAATTTATGATGAGGTAAATATCCAAATA 960
QY 859 GGCAATTAACCTGAATCTTACAAGAGAATAATTTATCAACTGAATAAATTTTGAACCGCTTT 918
DB 961 GGTGTCNAATCTGAATCTTACTCGAGAATTTAT-----CAGGTACTTAATCTCGAGA 1013
QY 919 ACTTACCTTGAATTTCAACCCAAATCTCGCTATAATGGAATATAATTTAAACAGTTTCAGGG 978
DB 1014 AAGCCCTTATAATATTATGACTTTCAATATCAAGAGGATTCACCTTACACGTAGACCGCA 1073
QY 979 CTTAGATTATTTTCATTTTATGATGAACTTATATTTATACAAAATGAAACGTACGGG 1038
DB 1074 TTTATTTACTTTGGCTTGATTTCTTTGAATTTTATGAAAAGCGCAAACTACTCTCTAATAA 1133
QY 1039 AATCGTTTATGTTGGTATTCGAAATCGTAATAGATCTACTTT-ATGCTACGACAGGAATGA 1097
DB 1134 TTTTTCACAGCCATTAATAATGTTTCATTACACCTTGATATATATATATATATATATATAT 1193
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DB 1194 TAGTGTTTTGGAAATCACAATGTAATGATAAATTTAAATCTCTTGGTTGGCAACAAA 1253
QY 1158 CTATAAGTTTCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1217
DB 1254 TATTATATATTTTATTAATGTCATAGCTTATGATTAATAATATCAATATCAATGATTAATA 1313
QY 1218 ATACTTTTCAATTAATCAATTTGAATCTTTATTAATAATTAATCACCCTAGTAAATTAATAC 1277
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QY 1278 ATATTTCAGCTGGGGGAAATTTATCTAATGATATAAAAAAACAACCTGATTTCAATTTCTGT 1337
DB 1374 TACAGCAGGATCTGGGCAAAATTAATCTATGATGATAAATAAATAATTTTCGGGTAACTAAT 1433
QY 1338 AAAAAAGACTGTAAACCAATTTAATTAATCCAAATTTGTTTACCAGCTATATATAGTTATAG 1397
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DB 1434 TCTTAAACCAAGAGAGAGAAATCAAGCAATCCCTACCCTTTTCCAAACATATGATAACTATAG 1493
QY 1398 TCATATTTTATCCAGTTTCTTTTATTAATTTATTTCTTATATAAATTTGGATTAGCGCTAAA 1457
DB 1494 TCATATTTTATCATTTTATTAATAAGTCTTAGTATCCC-----TGCNACATA 1538
QY 1458 TATATTATATACAGGTCGATTTAGGATGGACACACAGTAGTGTGTTAATAGAAATTAATCAAT 1517
DB 1539 TAAACCTCAAGTGTATACGTTTCTTGGACACACTCTAGTGTGATCCTAAAAATACAAT 1598
QY 1518 ATCAGATAAAATTAATTAATGATCCAGCAATCAAAAGGTAAACAGTCTTGTATACAACTC 1577
DB 1599 TTATACACATTTAACTACCCAAATTCAGCTGTAAAAAGCGAATTCACCTGGGACTGCTTC 1658
QY 1578 TAGGTAATTTGAAGGACCTGCTCATACAGGAGGAACTCTGTTTATTTTACAAAGTCAAGG 1637
DB 1659 TAAGGTTGTTTCAAGGACCTGCTCATACAGGAGGGAATTAATGATTTTCAAGATCA--- 1715
QY 1638 GCGTTTAGAGATTACATGTAGAACTCTCTAATTTCTACAAATCTTTATTTACATTTAGCTCG 1697
DB 1716 ---TTTCAAAATTTACATGTCAACACTCAATTTTCAACATCTGTTTATATAAGAAATCG 1772
QY 1698 ATACGCTCAAAATTTGGTCTGGAATACTCTTCTTAATATATATCTTTTACAAATACCAGAGT 1757
DB 1773 TTATGCTTCAATTTGAAGCGCAAAATACACGAGCTGTTATAAATCTTAGTATCCCAAGGG- 1831
QY 1758 AATAGGATACCACCTCAACGACTCAACACACTTTTCTGTTGTTTATATAATAATTAATTT 1817
DB 1832 --TAGCAGAACTCGGTATGCACTCAACCCCACTTTTCTGTTACAGATTTATCGAATTT 1889
QY 1818 ACAATACGAGATTTTGGGTATTTCCAAATTTCCAAATTTCCAAATTTACATTTTAAATTCG 1877
DB 1890 AATAATTAAGATTTTTCAGTACTTAGAATTTTCTACGAGGTGAAATTTGCTCCAAATCA 1949
QY 1878 AAACATACCAATTTATATTTTAAATCGTGAGATGAT---CAAATTTCAATTTTAAATCATGA 1934
DB 1950 AAACATATCTCTTGTGTTTAAATCGTTCGATGATATATACAAACACACAGTACTTATTGA 2009
QY 1935 TAAATTTGAATTTATACCAATTTACTCTCTGTCAGCCAAATAGAGAGAGAGAGAGAGAGAG 1994
DB 2010 TAAATTTGAATTTTCTGCCAATTTACTCGTTCTATAGAGAGGATAGAGAGAGAGAGAG 2069
QY 1995 AGAACTATCAAAACAAAAATAAATATACATTTTTCACAAATCATACAAAAATACCTTTAAA 2054
DB 2070 AGAAACAGTACAAATTAATTAATATATATTTTATGCAATCTTATATAAABACACTTTACA 2129
QY 2055 TATAGAAGCCCAAACTATGATATTGATTA 2085
DB 2130 ATCAGAACTTACAGATTATGACATAGATCA 2160
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RESULT 3

US-09-224-024-30

; Sequence 30, Application US/09224024

; Patent No. 6056953

; GENERAL INFORMATION:

; APPLICANT: Leslie Hickie

; APPLICANT: Jewel Payne

; TITLE OF INVENTION: Materials and Methods for the Control of

; TITLE OF INVENTION: Calliphoridae Pests

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,024
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-224-024-30

Query Match          7.6%; Score 158; DB 3; Length 2061;
Best Local Similarity 48.3%; Pred. No. 4.3e-22;
Matches 999; Conservative 0; Mismatches 895; Indels 174; Gaps 13;

QY      2  TGTGTCGAAGGGAATACACATATATGGTGATTAATTCGAGACATTTGCTAGTGTGATACAA 61
DB      149  TGTGTCGAAGTAATCAACAATATGGCAATATGCGGGGAATTTGTAGTCTCGAACTA 208

QY      62  TTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTGTAGCCGGTATAGTGGGC 121
DB      209  TTGTTGGAGTTAGTGCAGGTATTATTGTAGTAGGAACTATGTTAGGAGCTTTTGTGCGCC 268

QY      122  TCACCTCTATATCCGGACCATAGGAATAATAGGTGCTATTAATATCTTTTGGTACCC 181
DB      269  -----CTGTCTTAGCTGCAGGTATAATATCTTTTGGAGCTT 304

QY      182  TAATCACTGCTTTTGGCCCGGGAGAACACAGCAAAACAGATATGACACAAATTTATTA 241
DB      305  TGTGTCGGATCTTTTGGCAAGGATCTGACCCCTG---CAATGTTTGGCAGGATTTGTTAA 361

QY      242  AAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATATAAACAGCTAAAGTTAC 301
DB      362  ACATCGGAGGAGCCCTATACAGAAATAGATAAAACATAATTAATGTACTAACTT--- 418

QY      302  AAACCTTAGAAGGATTTAGCAAAATATTACAAAGCTATTAATACAGCATTAGATGGGA 361
DB      419  ---CTATCGTAAACACCTATAAAATAATCAACTTGTATAAATATCAAGAAATTTTTCGATAAAT 475

QY      362  GAAAAATTAAGACACTACAGCTCTCGGATTACCAATCATCAGCATTAACACAGCTG 421
DB      476  GGAGCGCAGCAGTACACAGCTTAATGCTTAAGCAGTA-CATGATCTCTTTACTACCTTA 534

QY      422  CCTTGACTCTTAAATACGATTGAGATGTTCCACAATGATTTTATTCGAGAAATACCTG 481
DB      535  GAACCTATAATAGATAAAGATTTAGATATGTTAAATA----- 571

QY      482  GTTTCCAACTTGAACCTTATAAACGCTATTACTACTATTATGCGCAAGCTGCTAAAT 541
DB      572  -----ATAATGTAGCTATCGAATAACCAACTCCCTCGAATGACAAATAGCTACTT 625

QY      542  TTCATTTAAATTTATTACAAAGGTGCTGAAATTTGGCTGATGAATGGAATGCGAGATATAC 601
DB      626  GGCACCTTGAATTTATTAAACATGCTGCTACCTATTACATATATGGCTGCAAAATCAAG 685

QY      602  ATCCTTTCAAAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATAAATCTTTAAAG 661
DB      686  GT-----ATAAATCCAAGTACTTTCAATTCATCTAATTACTATCAGGGGCTATTTAAAC 739

QY      662  ABAATATACCTTAATAGTAACCTATTGTGCAATACCTATAGAAGGAGGACTAAATAAAC 721
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QY      782  TTACTGTATTAGATACTACTCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATT 841
DB      860  TAACTGTGTAGATCTTATTGTCTATTTTTCCAAATTTATGACCCAGAAAAATA----- 911
QY      842  CAATAGGAAGATAGTGGCATTAAACCTGAACCTTACAAGAGAGAAATTTTATACAACCTGAA 901
DB      912  -----TCAATAGAGGATTAATCTGAACCTTACCAGAGAGAGTTTATACGATGTTA 961
QY      902  TAAATTTTGACCGTCTTACTTACCTTTGAAATTCACCCCAATCTCGCTATAAATGGAATATA 961
DB      962  -----ATTCAATACATATTAGAACCAATAACAGAACTAGAAA 997
QY      962  ATTAAACAGTTTCAGGGCTTAGATTTATTTTCAATTTTAGATGAATTTATTTTATACAA 1021
DB      998  ATGGATTAACTAGAAATCCTACATTTATTCTTGGATAAACCAAGGGCGTTTTCACAA 1057
QY      1022  AAAATGAAACGTACGGGAATCGTTTAGTTGGTATTTCGGAATCGTAATAGATCTACTTATG 1081
DB      1058  GAAATTTCTCGAGACATCTTGTATCCTTATGATATTTTCTTTTACAGGTAAACCATGG 1117
QY      1082  CTACGACAGGAACCTGAAATTTATATATGAGAGAAAGAACAGTCCACCCACAAACAAAACCTT 1141
DB      1118  CCTTTAGACATACTAATGATGATCGCAACATAATCTGGGGAGCGGTTTCATGGACATATTA 1177
QY      1142  TAATACCATTTGAAATCTCTATAAAGTTTCAATTTGTAACGTAGATAGCAAGTAACTCCTACTT 1201
DB      1178  TTTCTCAAGACACATCCAAAGTATTTCCTTTTATAGAAACAAACCTATTGTAAGGTGCG 1237
QY      1202  CCCCTTTTCTCAACATATACTTTTACAAATTAATCAAAATGCAATCTTATTATAAATAATTCAC 1261
DB      1238  AAATTTGTGACATAGAGAGTACTCAGATATAATATATGAAATGATATTTTTCGAAATA 1297
QY      1262  CTAGTAATAAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATAAAAAACAACTG 1321
DB      1298  GCAGTGAAGTATTTTCGATATTCATCCAATTCACCAATAGAAAAATAATTTATAAAGAACTG 1357
QY      1322  ATTTTCAATTTCTGTAAAAAAGACTGTAAACCAATTTAATCCAAATTTGTTTACCAA 1381
DB      1358  ATTTCTTATATGATTTCCAAACCAACATGGAATAAATAAGAAATGTCATCTCTATCGT 1417
QY      1382  GCTATAATAGTTATAGTCAATTTTATCCAGTTTCTTCTTATTATTATTATTCCTATAAAA 1441
DB      1418  ATATAAATACTGATTAATATATATTTTC----- 1445
QY      1442  TTGGATTAGCGCTAAATATATTATATACAGGTGCAATTTAGGATGGACACACAGTAGTGTTA 1501
DB      1446  -----AGTAGTTAGAGAAAGAAAGAGAGTTGCAATTTAGTTGGACACATACCTAGTGTG 1498
QY      1502  ATAGAAATTAATGCAATATCAGATAAATAATTAATTTACATGATCCCAATTCAGAGGTAACA 1561
DB      1499  ATTTCCAAATAACATAGATTTTAGATAACATCACCCAAATCCACGCTCTTAAAGCTTTGA 1558
QY      1562  GTCTTGATACAAACTCTTAAGGTAATTTGAAGGACCTGGTTCATACAGGAGGAAACTTGGTTT 1621
DB      1559  AGTGAAGTTCTGATTTGGAATAATTTGGAAGGTCCTGGTCACACAGGTGAGACTTGGTAA 1618
QY      1622  ATTTACAAAGTCAAGGGCGTTTAGAGATTAATGATAGAACTCCTTAATTTCTACAAATCTT 1681
DB      1619  TTTCTTAAAGATAGTAGTGGATTTTAGAGTTAGATTTTAAATAAATGTTTCTCGACAAAT--- 1675
QY      1682  ATTACATTAGACTTCGATACGCTCAAAATGGTCTGGAAATATCTCTTCCATAATATCTC 1741
DB      1676  ATCAAGTAGCTATTCGTTATGCTACTAATGCTCCCAAGAACAAACAGTA--TTCTTAACCGG 1733
QY      1742  TTACAATACCGAGGTAAATAGGAATACCACTCAACGACTCAACACACTTTTCTCGGTA 1801
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Db 1734 AATAGATCTATTAAGTGTGGAGCTCCCTAGTACCACTTCCGCCAAAAC-----C 1783
 Qy 1802 CAAATATTATAATTTTACATCGGAGATTTTGGGTATTTCCAAATTTCCAAGTACAGT-- 1859
 Db 1784 CAAATGCTACAGATTTTAAACATATGCGAGATTTTGGATATGTAACATTTCCAAGAACAGTTC 1843
 Qy 1860 -----AACATTTACCTTTTAAATCGAACAATACCATTTATTTAATCGTGCAGATGTAT 1912
 Db 1844 CAAATAAAACATTTGAAGGAGAGACACTTTTAAATGACCTTATATGGTACACCAATC 1903
 Qy 1913 CAAATTCAAATTTTAAATGATAAAATTTGAATTTTATACCAATTTCTCTGTAGGCC 1972
 Db 1904 ATTCAATATATATATATTTGACAAATCGAATTTTCCAAATCCTCAATCTGTATTAG 1963
 Qy 1973 AAAATAGAGAAAAACAAAATTTAGAACTATCCAAACAAAATAAATACATTTTTCACAA 2032
 Db 1964 ATTATACAGAGAGCAAAATATAGAAAAAACAAGAAATAGTGAATGATTTTATTTGTTA 2023
 Qy 2033 ATCATCAAAAATACTTTTAAATATAGA 2060
 Db 2024 ATTAAAACAAAGTCTTTACTATAAATAGA 2051

RESULT 4

PCT-US94-07902-30
 ; Sequence 30, Application PC/TUS9407902
 ; GENERAL INFORMATION:
 ; APPLICANT: 4980 Carroll Canyon Road
 ; APPLICANT: Street address:
 ; APPLICANT: City: San Diego
 ; APPLICANT: State/Province: US
 ; APPLICANT: Country: 92121
 ; APPLICANT: Postal code/Zip:
 ; APPLICANT: Phone number: (619) 453-8030 Fax number: (619) 453-6991
 ; APPLICANT: Telex number:
 ; TITLE OF INVENTION: Materials and Methods for the Control of
 ; TITLE OF INVENTION: Calliphoridae Pests
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David R. Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/07902
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saliwanchik, David R.
 ; REGISTRATION NUMBER: 31,794
 ; REFERENCE/DOCKET NUMBER: MA79
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 904-375-8100
 ; TELEFAX: 904-372-5800
 ; INFORMATION FOR SEQ ID NO: 30:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2061 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; PCT-US94-07902-30

Query Match 7.6%; Score 158; DB 6; Length 2061;

Best Local Similarity 48.3%; Pred. No. 4.3e-22;

Matches 999; Conservative 0; Mismatches 895; Indels 174; Gaps 13;

Qy 2 TGTGTCACGGGAATACACAATATGGTGATAATTTTCGAGACATTTGCTAGTGTGATACAA 61
 Db 149 TGTGTCACGATATCAACAATATGGCAATATGCGGGGAATTTTGTAGTCTTGAAACTA 208
 Qy 62 TTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTCTGTAGCCGGTATAGTGGGC 121
 Db 209 TTGTTGGAGTTAGTGCAGGTATTATTGTAGTAGAACTATGTTAGGAGCTTTTGTGCCCC 268
 Qy 122 TCACITCTATATCCGACCGATAGGAATTAATAGGTCTATTAATAATATCTTTTGGTACCC 181
 Db 269 -----CTGCTTAGCTGAGGTATTAATCTTTTGGGACTT 304
 Qy 182 TAATCACTGCTTTTGGCCCGCGGAGAACAAACAGATATGGACACAATTTTATTA 241
 Db 305 TGTGCGGATCTTTTGGCAAGGATCTGACCTG---CAATGTTTGCAGGATTTGTTAA 361
 Qy 242 AAATGGGAGAAATTTTGTGTATACACCGTTTAAACAGAAAGCATAAACAGCTAAAGTTAC 301
 Db 362 ACATCGGAGGAGCCCTATACAAAGAAATAGATAAAACATAATTAATGTACTAATCTT--- 418
 Qy 302 AAATTTTAGAAGGATTTAGCAAAATATTACAAAGCTATATACAGCATTAGATGATTGGA 361
 Db 419 ---CTATCGTAAACACCTTATAAAATAATCAACTTGATAAATATCAAGAAATTTTTCGATAAT 475
 Qy 362 GAAAAATTAAGAGACTACAAAGCTCTCGGATTACCAACCATCATCAGCAATTACAACAGCTG 421
 Db 476 GGGAGCCAGCAGTACACAGCTTAATGCTAAAGCAGTA-CATGATCTCTTTTACTACCTTA 534
 Qy 422 CTTGACTCTTAAATAACGATTTTGAGAAATGTTTCAATGATTTTATTCGAGAAATACCTG 481
 Db 535 GAACCTATATAGATAAAGATTTAGATATGTTAAAA----- 571
 Qy 482 GTTTCGAATTTGAACTTATAAAGCGTATTACTACCTATTATTATCGCAAGCTCTAATT 541
 Db 572 -----ATAATGCTAGCTATCGAATACCAACACTCCCTCGCATATGCAAAATAGCTACTT 625
 Qy 542 TTCATTTAAATTTTATCAACAAGGTGCTGAAATGGCTGATGAATGGAATGCAGATATAC 601
 Db 626 GGCACITGAAATTTTATTAACAATGCTGCTACTCTATTAACAATATATGCTGCAAAATCAAG 685
 Qy 602 ATCCTTCACAAATTTGAACCTTAATGCTGGAAATCATCAGATGACTATTATAAATTTTAAAG 661
 Db 686 GT-----ATAATCCAAGTACTTTCAATTTCTAATTTACTATCAGGGCTATTAAAAAC 739
 Qy 662 AAAATATACCTTAATATAGTAATTTGTCGAATATCTATAGAGAGGACTAATATAAC 721
 Db 740 GTAAATACAAAGATATATGACTATTGTATACAAACGTACAATGCAGGACTAACTATGA 799
 Qy 722 TTCGAACGACCTTAATATGAGATGGAGTATTTAATGATTAATCGAAGATATATGACTA 781
 Db 800 TTGAAGTAACTACTAAACGCAACATGGAATATGTAATATCTTACCGTTTAGAATGACTC 859
 Qy 782 TTACTGTATTAGATCTATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATT 841
 Db 860 TAATGTTTGTAGATCTTTATGCTATTTTCCAAATTTATGACCCAGAAAAATA----- 911
 Qy 842 CAATAGGAAGAAATAGGTGGCAATTAAGAACTGAACCTTCAAGAGAAATTTATACAACTGAA 901
 Db 912 -----TCCAATAGGAGTTAAATCTGAACCTTACCAGAGAAAGTTTATACGAATGTTA 961
 Qy 902 TAAATTTTGACCGCTTTACTTACCTGAAATTTCAACCAATCTCGCTATAATGGAATATA 961
 Db 962 -----ATTCAGATACATTTAGAACCAATAACAGAACTAGAAA 997
 Qy 962 ATTTAAACACGTTTCAAGGCTTAGATTATTTTCATTTTGTAGTAACTTATATTTTATACAA 1021
 Db 998 ATGGATTAACCTAGAAATCTACATTTATCTTGGATAAAACCAAGGGGGTTTTACACAA 1057
 Qy 1022 AAAATGAACGTAACGGGAATCGTTTGTGATTTGGAATCGTAATAGATCTACTTATG 1081
 Db 1058 GAAATTCGAGACATTTCTTGATCCTTATGATATTTTTTTTCTTTTACAGGTAACCAAGATGG 1117

Qy	1082	CTACGACAGGAACTGAAATTTATATATATGAGAGAAAGAACAGGTCCACCCACAAACAAACTT	114
Db	1118	CCTTTACACATCAATTAATGATGATCGCAACATAATCTGGGGAGCGGTTCAATGGACATATTA	1177
Qy	1142	TAATACCAATTTGAAATCCTATAAAGCTTTCAATTTGTAACTGTATAGACAAGTAACCTCTACTT	1201
Db	1178	TTTTCTCAAGACACATCCAAAGTATTTCTTTTATAGAAACAAACCTATTGTATGAAGTCG	1237
Qy	1202	CCCCTTTTCTTAAACATATACCTTTTACAATTAATCAAAATGAACTTTATTTAAATAAATTCAC	1261
Db	1238	AAATTTGTACAGACATAGAGAGTACTCAGATATAATATATGAAATGATATTTTTTTTCGAATA	1297
Qy	1262	CTAGTAATAAATTAACATATTTTCCAGCTGGGGGAATTTATCTAAATGATAAAAAACAACACTG	1321
Db	1298	GCAGTGAAGTATTTTCGATATTTTCACTCCAAATCCAAACATAGAAAATAATTTATAAAGAACTG	1357
Qy	1322	ATTTTCAATTTCTGTAAAAAAGACGTGTAAACCAATTTATTAATCCAAATTTGTTTACCAA	1381
Db	1358	ATTTCTATATGATTTCCAACACACATGGAATAATGAAGTATATGCTCATCTATCGT	1417
Qy	1382	GCTATAATAGTTATAGTCATATTTTATCCAGTTTTCCTTTATTTAAATTTTCTCTATAAAA	1441
Db	1418	ATATAAAAACTGATAATATATATTTTC-----	1445
Qy	1442	TTGGATAGCGCTAAATATATATATACAGGTGCAATTAGGATGGACACAGAGTAGTGTA	1501
Db	1446	-----AGTAGTTAGAGAAAGAGAGAGTTGCAATTTAGTTTGACACATACTAGTGTTG	1498
Qy	1502	ATAGAAATAATGCAATATCAGATAAAAATAATTAACAATGATCCCCAGCAATCAAAGGTAAACA	1561
Db	1499	ATTTCCAAATAACAATAGATTTTAGATAACATCACCCAAATCCACGCTCTAAAAGCTTTGA	1558
Qy	1562	GTCCTTGATACAACTCTAAGGTAAATTGAAGGACCTGGTCATACAGGAGGAAACTTTGGTTT	1621
Db	1559	AGGTAAGTTCTGTATTCGAAAAATTTGTGAAGGCTCCTGGTCACACAGGTGGAGACTTTGGTAA	1618
Qy	1622	ATTTTACAAAGTCAAGGGCGTTTAGAGATTTACATGTAGAACTCCTTAATTTCTACACAATCTT	1681
Db	1619	TTCTTAAAGATAGTATGATGATTTTAGAGTTAGATTTTAAAAATGTTTCTCGACAAAT---	1675
Qy	1682	ATTACATTAGACTTTCGATACGCTACAAATGGTGTGGAAATPACTCTTCTTAATATATCTC	1741
Db	1676	ATCAAGTACGTATTTCGTTATGTCTACTAATGCTCCAAAGACAAACAGTA--TTCTTAACCGG	1733
Qy	1742	TTACAATACAGGATTAATAGGAATACCACTCAACGACTCAACAAACACTTTTCTGTGTA	1801
Db	1734	AATAGATACTATAAGTGTGGAGCTCCCTAGTACCCTTCGCGCCAAAC-----C	1783
Qy	1802	CAAAATTAATAATTTTACAATACGGAGATTTTGGGTATTTTCCAAATTTTCCAAGTACAGT--	1859
Db	1784	CAAAATGCTACAGATTTTAAATATGACATATTCAGATTTTGGATATGTAACATTTTCCAAAGACAGTTC	1843
Qy	1860	-----AACATTACCTTTTAAATCGAAACATACCATTATATTTAAATCGGTGCGAGATGTAT	1912
Db	1844	CAAAATAAAACATTTGAAGGAGAACACACTTTATTAATGACCTTATATGGTACACCAAATC	1903
Qy	1913	CAAAATTCAAATTTTAAATCAATGATAAATTTGAAATTTATACCAATTTACTCTCTGTACGCC	1972
Db	1904	ATTCATATAATATATATATTGACAAAATCGAATTTTATTTCCAATCACCTCAATCTGTATTAG	1963
Qy	1973	AAAAATAGAAAAACAAAAATTAGAAACTATCCAAACAAAAATAAATACATTTTTTTCACAA	2032
Db	1964	ATTATACAGAGAACAAAATATAGAAAAAACACAGAAAAATAGTGAATGATTTATTGTTTA	2023
Qy	2033	ATCATACAAAAAATCTTTAAATATAGA	2060
Db	2024	ATTAACAAAGTTCTTACTAAAAATAGA	2051

; GENERAL INFORMATION:
 ; APPLICANT: Michaels, Tracy Ellis
 ; APPLICANT: Fonceerrada, Luis
 ; APPLICANT: Narva, Kenneth E.
 ; TITLE OF INVENTION: Process for Controlling Scarab Pests
 ; TITLE OF INVENTION: with Bacillus thuringiensis Isolates
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David R. Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/08/315,468
 ; APPLICATION NUMBER: US/08/315,468
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/014,941
 ; FILING DATE: 01 FEB 1993
 ; APPLICATION NUMBER: 07/828,430
 ; FILING DATE: 30-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/808,316
 ; FILING DATE: 16-DEC-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saliwanchik, David R.
 ; REGISTRATION NUMBER: 31,794
 ; REFERENCE/DOCKET NUMBER: MA73.C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 904-375-8100
 ; TELEFAX: 904-372-5800
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3507 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Bacillus thuringiensis
 ; STRAIN: kumamotoensis
 ; INDIVIDUAL ISOLATE: 50C
 ; IMMEDIATE SOURCE:
 ; LIBRARY: LambdaGEM-11(tm) library of L. Fonceerrada
 ; CLONE: 50C(b)
 ; US-08-315-468-3

	Query Match	4.4%	Score 92.6	DB 2	Length 3507
	Best Local Similarity	44.7%	Pred. No. 3.5e-09		
	Matches 683	Conservative 0	Mismatches 784	Indels 60	Gaps 6
QY	429	TCCTAAAAATACGATTTTGAGAAATGTCACAAATGATTTTATTTCGAGAAATACCTGGTTTCCA	488		
DB	504	TGTTCGAAATCGAATTTTGAATTCCTGGATAGTTTATTTCGCAATATATATGCCATCTTTTCG	563		
QY	489	ACTTGAACCTTATAAAACGCATTTACTACCTATTTATGCGCAAGCTGCTAAATTTTCATTTT	548		
DB	564	AGTGACAAATTTTGAAGTACCATTCCTTACAGTATATACAATGCCAGCAACCTACATTTT	623		
QY	549	AAATTTATTACACACAGGTGCTGAAATGGCTGATGATGGAATGCAGATATACATCCTTC	608		
DB	624	ACTTTTATTAAAGGACGCATCAATTTTGGGAAGAATGG-----	663		
QY	609	ACAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATAAACTTTTAAAGAAATAT	668		

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Db 664 -----GGATTCTTCAAGCACTATTAACTACTACTATTAATCGTCAATGAACTTAC 716
Qy 669 ACCTAATATAGTAATCTATTGTGCAATACCTATAGAGAGGAGCTAAATAACTTCGAAA 728
Db 717 TGCAGAAATATCTGACCACTGTGTAAAGTGGTATGAACTGGTTAGCAAAATTAAGG 776
Qy 729 CGAACCTAATATGAGATGGAGTATATTAAATGATATCGAAGATATATGACTATTAAGT 788
Db 777 CTCGAGCGCTAAACAATGGGATGACTATAACCAATTCGCTAGAGAAATGACATGACGGT 836
Qy 789 ATTAGATACCTATCGCTCAATTTTCTTTTATATGATATAAAGAGATACAAAGATTCATAGG 848
Db 837 GTTAGAGCTGTGTCATTAATTTTCAACTATGATACGCTACGT-----ATCCACTGGC 890
Qy 849 AAGAAATAGTGGCATTAATAAAGCTGAACTTCAAGAGAAATTTTATACAACTGAAATTAATTT 908
Db 891 AACACAGCTCAGCTTACAAGGGAAGTATATACAGATCCACTTTGGCGCGTAGATGTGCC 950
Qy 909 TGACCGCTTACTTACCTTCAAAATTCACCCCAATCTCGCTATTAATGGAATATAATTTAAC 968
Db 951 TAATATTGGCTCTGGTATGACAAAGCACCTTCTTCTCAGAAATAGAAAAGCGGCTAT 1010
Qy 969 ACGTTACGGCTTATGATTAATTTTCAATTTTAGATGAATCTTATATTTTATACAAAAATGA 1028
Db 1011 TCGTCCACCTCATG---TGTTGATTAATATAACGGGACTCACAGTTTATACAAAAAAGC 1067
Qy 1029 AACGTACGGGAATCGTTAGTTGGTATTTGCGAATCGTAATAGATCTACTTATGCTACGAC 1088
Db 1068 TAGCTTCACT--TCTGATCGTTATATGAGATATTGGGCTGTGTCATCAATAAGCTATAAG 1125
Qy 1089 AGGAACCTGAAATATATATGAGAGAAAGACAGGTCACCCACACAAACAACTTTTAATACC 1148
Db 1126 CATATCGGTACGAGTAGTACCTTTTACACAGATGATGGAACCAATCAAAATTTTACAAGT 1185
Qy 1149 ATTTGAATCTTATAAAGTTTCAATTTGTAACGTAGACAACTACTCTCTCCCTTT 1208
Db 1186 ACTAGCAATTTTGAATTTACGAAATACGATATTTTACAGACTTTTCAATATGTTGACGTA 1245
Qy 1209 TCCTAACATATACCTTCAATTAATCAAAATGAACTTTTATTAATAATTAATCACCCTAGTAA 1268
Db 1246 CTCCTGATATAGTTTACCCTGGTTATACGTATATACATTTTGTGAATGCCAGAAACCGAG 1305
Qy 1269 TAAATTAACATATTCAGCTGGGGGAATTTATCTAATGATATAAATAAATAAATACTGATTTCA 1328
Db 1306 TTTTATATGTTAAATCAATTTGAATTAATACCAAGAAAGAGCTTAACGTATAAACCCAGCTTC 1365
Qy 1329 ATTTCTGTAAATAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCAGCTATAA 1388
Db 1366 AA-----AGATATTATAGATCGGCAAGAGATTCGGAATTAGAATTTGCTCCAGAACTTC 1421
Qy 1389 TAGTTATAGTCATATTTTATCCAGTTTCTTTTATTTAATTTATTTCTATAAATTTGGATT 1448
Db 1422 AGGTCACCAATTTACGAGTCATATAGCCATAGATTAGGTATATATTTTATTTTACTC 1481
Qy 1449 AGCGTAAATATATATATACAGGTGCAATTAGGATGGACACACAGTAGTGTATATAGAAA 1508
Db 1482 CAGTTTCAACTAGCAGCTATGTACCTGTATTTTCTTGGACATCGGAGTCGAGATCTAAC 1541
Qy 1509 TAATGCAATATCAGATAAATAATTTACAAATGATCCAGCAATCAAAAGGTAACAGCTTTGA 1568
Db 1542 AAAATACAGTTTAAAGTGGCGAAATCACCCAAATACAGGGGCAAGCTTAGCACCATAGG 1601
Qy 1569 TACAACTCTAAGGTAATTTGAAGGACCTGGTCATACAGGAGGAACTTTGGTTTATTTACA 1628
Db 1602 CAGAAATACTTATATAATAAAGGGCGTGGTTATATACAGGGGAGACTTTAGTGGCTTTAAC 1661
Qy 1639 AAGTCAAGGGCGTTTATAGATTTACATGATAGAACTCTTAATTTCTACAAATCTTATACAT 1688
Db 1662 GGACCGCATCGGAAGTGTGAGTTTCAGATGATCTTTCCAGAGTCTCAACGATTCGGTAT 1721
Qy 1689 TAGACTTCGATACGCTACAAATGGTGTGGAATACTCTCTCTAATATATCTCTTACAAT 1748
1722 TCGGATTCTAGCTTCTTAATGAAACTAGTTATA-----TTAGTTT 1763
1749 ACCAGAGTAATAGGAATACCCTCAACGACTCAACAAACACTTTTCTGGTACAAATTA 1808
1764 ATAGGACTATACCAAAAGCGGAACTTTAAATTCACACGACATATCTTAATAAAATGA 1823
1809 TAATAATTTACAAATACGGAATTTTGGGTATTTTCCAAATTTTCCAAGTACAGTAACATTACC 1868
1824 AAATGATTTTAAACATATAATGATTTTCAATATATAGAAATATCCAAAGAGTCAATTTTCAGTAAA 1883
1869 TTTAAATCGAAACATACCATTATTTATTTAATCGTGAGATGTATCAAAATTTCAATTTTAAAT 1928
1884 TGCTTCTTCAACATACAGAGGTTATCTATAGGTATACAAACGAAATTAATTTATTTAT 1943
1929 CATTGATAAAATGAAATTTTATACCAAT 1955
1944 TTTAGACCGAATCGAATTCATCCAGT 1970
RESULT 6
US-08-349-867-22
; Sequence 22, Application US/08349867
; Patent No. 5508264
; GENERAL INFORMATION:
; APPLICANT: Bradfisch, Gregory A.
; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: No. 5508264el Pesticidal Compositions
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,867
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-349-867-22
Query Match 3.8%; Score 79.6; DB 2; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;
Qy 436 ATACGATTTGAGAATGTTTCAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGA 495
Db 388 ATTGATTTGCTAATACAGACGAGCTTTAATAACAGCAATAATAATTTTACACTTACA 447
Qy 496 ACTTATAAAACGCTATTACTACTTATTTATGCGAAGCTGCTAATTTTCAATTTAAATTA 555
Db 448 AGTTTGAATCCCTCTTTTATCGGTCTATGTTCAAGCGCGGAATTTACATTTTACTACTA 507
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496	ACTTATATAAAGCGCTATTACTACCTATTATTATGCGCAAGCTGCTCAATTTTCATTTAAATTTA	555
448	AGTTTGGAAATCCCTCTTTTATCGGTCTATGTTCAAGCGCGGAATTTACATTTATCACTA	507
556	TTACAACAAGGTGCTGAATGGCGTGATGAATGGAATGCAGATATACATCCTTCCACAAATT	615
508	TTAAGACGCGCTGTATCGTTTGGCAGGGTTGGGACTGGATATAGCTACTGTTAATAAT	567
616	GAACTTAATGCTGGAAACATCAGATGACTATTATATAAAGCTTTTAAAGAAATAATATACCTAA	675
568	C-----ATTATAATAGATTAATAAATCTTATTTCATAGA	600
676	TATAGTAACATTTCGTGCAATACCTATAGAGAGGAGCTAAATAAACTTCGAAACGAACCT	735
601	TATACGAAACATTTGTTGGACACATACAACTCAAGGATTGAAAACTTTAAGAGGTACTAAT	660
736	AATATGAGATGGAGTATATTAAATGATTATCGAAGATATATGACTATTACTGTATTAGAT	795
661	ACTCGAANAATGGGCAAGATCAATCAGTTTAGGAGAGATTTAAACACTTACTGTATTAGAT	720
796	ACTATCGCTCAATTTTCTTTTTATGATATAAAGAGATA	833
721	ATCGTTGCTCTTTTTCCGAACCTACGATGTTAGAACATA	758

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RESULT 9
US-08-239-476-26
; Sequence 26, Application US/08239476
; Patent No. 5527883
; GENERAL INFORMATION:
; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; TITLE OF INVENTION: Pseudomonas Fluorescens
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSES: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-239-476-26

Query Match      3.8%; Score 79.6; DB 2; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

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388	ATTCGATTGCTAATACAGACGCGCTTTAATAACAGCAATAAATAATTTTACACTTACA	447
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448	AGTTTTGAATCCCTCTCTTTATTCGCTCTATGTTCAAGCGCGAAATTTACATTTATCACCTA	507
556	TTACAAACAAGGTGCTGGAATTTGCTCGATGGAATGCGAATATACATCTCTTCACAAATT	615
508	TTAAGAGAGCGTGTATCTGTTGGCGAGGGTTGGGACTCGATATAGCTACTGTTTAATAAT	567
616	GAACTAATGCTGGAAACATCAGATGACTATTATAAACTTTTAAAGAAAAATATACCTAAA	675
568	C-----ATTATAATAGATTATATAAATCTTTATTCATAGA	600
676	TATAGTAACATTGTGCAAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACT	735
601	TATACGAACATGTGTTGGACACATACATCAAGGATTAGAAAACCTTAAGAGGTACTAAT	660
736	AATATGAGATGGAGTATATTTTAATGAATATCGAAGATATATGACTATTACTGTATTAGAT	795
661	ACTCGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTTAAACACTTACTGTATTAGAT	720
796	ACTATCGCTCAATTTTCTTTTATGATATAAGAGATA	833
721	ATCGTTGCTCTTTTTCGGAACATACGATGTTAGAACATA	758

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Query Match      3.8%; Score 79.6; DB 2; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

QY 436 ATACGATTGGAGAAATGTTCCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAA 495
DB 388 ATTGCAATTTGCTATACAGACGACGCTTTAAATAACAGCAATAAATAATTTTACACTTACA 447
QY 496 ACTTATAAACGCTATTTACTACTATTTATTCGCGAAGCTGCTAAATTTTCATTAAATTTA 555
DB 448 AGTTTTGAAATCCCTCTTTTATCGGTCTATGTTCAAGCGCGAATTTTACATTTATCACTA 507
QY 556 TTACAACAAGGTGCTGAATTTGGCTGATGAATGGAATGGAATGGAATGGAATGGAATTT 615
DB 508 TTAAGAGACGCTGATCGTTTGGGACGCTGATGATGATGATGATGATGATGATGATGAT 567
QY 616 GAACCTAATGCTGGAACATCAGATGACTATTAATAAATTTTAAAGAAAATATACCTTAA 675
DB 568 C-----ATTATATAGATTAATAAATCTTATTCATAGA 600
QY 676 TATAGTAATCTATTTGCAAAATACCTATAGAGAGAGACTAAATAAATCTTGAACGAACT 735
DB 601 TATACGAAACATTTGTTGGACACATACAAATCAAGGATTAGAAAACCTTAAGAGGTACT 660
QY 736 AATATGAGATGAGATATTTAATGATTTATCGAAGATATATGACTATTTACTGTTATAGAT 795
DB 661 ACTCGACAATGGCAAGATTTCAATCAGTTTAGGAGAGATTTAAACACTTACTGTTATAGAT 720
QY 796 ACTATCGCTCAATTTCTTTTATGATATAAAGAGATA 833
DB 721 ATCGTTGCTCTTTTCCGAACTACGATGTTAGAACATA 758

RESULT 11
US-08-598-305A-26
; Sequence 26, Application US/08598305A
; Patent No. 5827514
; GENERAL INFORMATION:
; APPLICANT: BRADFISCH, Gregory A.
; APPLICANT: THOMPSON, Mark
; APPLICANT: SCHWAB, George E.
; TITLE OF INVENTION: No 5827514e1 Pesticidal Compositions
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/598,305A
; FILING DATE: 08-FEB-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/349,867
; FILING DATE: 06-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA86.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-598-305A-26

Query Match      3.8%; Score 79.6; DB 2; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

QY 436 ATACGATTGGAGAAATGTTCCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAA 495
DB 388 ATTGCAATTTGCTATACAGACGACGCTTTAAATAACAGCAATAAATAATTTTACACTTACA 447
QY 496 ACTTATAAACGCTATTTACTACTATTTATTCGCGAAGCTGCTAAATTTTCATTAAATTTA 555
DB 448 AGTTTTGAAATCCCTCTTTTATCGGTCTATGTTCAAGCGCGAATTTTACATTTATCACTA 507
QY 556 TTACAACAAGGTGCTGAATTTGGCTGATGAATGGAATGGAATGGAATGGAATTT 615
DB 508 TTAAGAGACGCTGATCGTTTGGGACGCTGATGATGATGATGATGATGATGATGATGAT 567
QY 616 GAACCTAATGCTGGAACATCAGATGACTATTAATAAATTTTAAAGAAAATATACCTTAA 675
DB 568 C-----ATTATATAGATTAATAAATCTTATTCATAGA 600
QY 676 TATAGTAATCTATTTGCAAAATACCTATAGAGAGAGACTAAATAAATCTTGAACGAACT 735
DB 601 TATACGAAACATTTGTTGGACACATACAAATCAAGGATTAGAAAACCTTAAGAGGTACT 660
QY 736 AATATGAGATGAGATATTTAATGATTTATCGAAGATATATGACTATTTACTGTTATAGAT 795
DB 661 ACTCGACAATGGCAAGATTTCAATCAGTTTAGGAGAGATTTAAACACTTACTGTTATAGAT 720
QY 796 ACTATCGCTCAATTTCTTTTATGATATAAAGAGATA 833
DB 721 ATCGTTGCTCTTTTCCGAACTACGATGTTAGAACATA 758

RESULT 12
US-08-639-923A-22
; Sequence 22, Application US/08639923A
; Patent No. 5840554
; GENERAL INFORMATION:
; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; TITLE OF INVENTION: Pseudomonas fluorescens
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,923A
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,476
; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83.D1
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-639-923A-22

Query Match      3.8%; Score 79.6; DB 2; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

Qy 436 ATACGATTGAGATGTTCAATGATTTTATTCGAGAAATACCTGGTTCCAACTTGAA 495
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 388 ATTCGATTTGCTAATACAGACGAGCTTTAATAACAGCAATAAATTTTACACTTACA 447
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 496 ACTTATAAACGCTATTACTACCTATTATGCGCAAGCTGCTAATTTTCAATTTTAAATTTA 555
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 448 AGTTTGAATCCCTCTTTTATCGGCTATGTTCAAGCGGGAATTTACATTTATCTACA 507
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 556 TTACAACAAGGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCTTCACAAATT 615
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 508 TTAAGAGAGCTGTATCGTTGGCAGGGTTGGGAGCTGGATATAGCTACTGTTAATAAT 567
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 616 GAACCTAATGCTGGAACATCAGATGACTATTATATAAATTTTAAAGAAAATATACCTAAA 675
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 568 C-----ATTATAATAGATTAAATAATCTTTATTCATAGA 600
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 676 TATAGTAACCTATTGTCGAAATACCTATAGAGAGGACTAAATAAATCTTGAACGAACCT 735
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 601 TATACGAAACATTTGTTGGACACATCAATCAAGGATTAGAAACTTAAGAGGTACTAAT 660
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 736 AATATGAGATGGAGTATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGAT 795
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 661 ACTGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTAAACACTTACTGTATTAGAT 720
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-08-639-923A-26
; Sequence 26, Application US/08639923A
; Patent No. 5840554
; GENERAL INFORMATION:
; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; PSEUDOMONAS FLUORESCENS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,923A
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,476
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; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-639-923A-26

Query Match      3.8%; Score 79.6; DB 2; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

Qy 436 ATACGATTGAGATGTTCAATGATTTTATTCGAGAAATACCTGGTTCCAACTTGAA 495
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 388 ATTCGATTTGCTAATACAGACGAGCTTTAATAACAGCAATAAATTTTACACTTACA 447
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 496 ACTTATAAACGCTATTACTACCTATTATGCGCAAGCTGCTAATTTTCAATTTTAAATTTA 555
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 448 AGTTTGAATCCCTCTTTTATCGGCTATGTTCAAGCGGGAATTTACATTTATCTACA 507
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 556 TTACAACAAGGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCTTCACAAATT 615
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 508 TTAAGAGAGCTGTATCGTTGGCAGGGTTGGGAGCTGGATATAGCTACTGTTAATAAT 567
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 616 GAACCTAATGCTGGAACATCAGATGACTATTATATAAATTTTAAAGAAAATATACCTAAA 675
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 568 C-----ATTATAATAGATTAAATAATCTTTATTCATAGA 600
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 676 TATAGTAACCTATTGTCGAAATACCTATAGAGAGGACTAAATAAATCTTGAACGAACCT 735
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 601 TATACGAAACATTTGTTGGACACATCAATCAAGGATTAGAAACTTAAGAGGTACTAAT 660
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 736 AATATGAGATGGAGTATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGAT 795
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 661 ACTGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTAAACACTTACTGTATTAGAT 720
Db ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
PCT-US95-05431-22
; Sequence 22, Application PC/TUS9505431
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: Street address: 5501 Oberlin Drive
; APPLICANT: City: San Diego
; APPLICANT: State/Province: California
; APPLICANT: Country: US
; APPLICANT: Postal code/Zip: 92121
; APPLICANT: Phone number: (619) 453-8030
; APPLICANT: Telex number:
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; PSEUDOMONAS FLUORESCENS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05431
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-05431-22

Query Match 3.8%; Score 79.6; DB 6; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

QY 436 ATACGATTGAGATGTTTACCAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAA 495
DB 436 ATACGATTGAGATGTTTACCAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAA 495
QY 388 ATTCGATTGCTTAATACAGACGCGCTTTAATAACAGCAATAAATAATTTTACACTTACA 447
DB 388 ATTCGATTGCTTAATACAGACGCGCTTTAATAACAGCAATAAATAATTTTACACTTACA 447
QY 496 ACTTATAAAACGCTATTACTACCTATTATGCGCAAGCTGCTAAATTTTCAATTTAAATTTA 555
DB 496 ACTTATAAAACGCTATTACTACCTATTATGCGCAAGCTGCTAAATTTTCAATTTAAATTTA 555
QY 448 AGTTTGAATCCCTCTTTTATCGGCTCTATGTTCAAGCGCGAATTTTACATTTACACTA 507
DB 448 AGTTTGAATCCCTCTTTTATCGGCTCTATGTTCAAGCGCGAATTTTACATTTACACTA 507
QY 556 TTACAAACAGGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCTTCCACAAAT 615
DB 556 TTACAAACAGGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCTTCCACAAAT 615
QY 508 TTAAGAGACGCTGATCGTTTGGCGAGGTTGGGACCTGGATATAGCTACTGTTAATAAT 567
DB 508 TTAAGAGACGCTGATCGTTTGGCGAGGTTGGGACCTGGATATAGCTACTGTTAATAAT 567
QY 616 GAACCTAATGCTGGAAACATCAGATGCTATTATAAACTTTTAAAGAAATATACCTAA 675
DB 616 GAACCTAATGCTGGAAACATCAGATGCTATTATAAACTTTTAAAGAAATATACCTAA 675
QY 568 C-----ATTATAATAGATTAAATAAATCTTATTCATAGA 600
DB 568 C-----ATTATAATAGATTAAATAAATCTTATTCATAGA 600
QY 676 TATAGTAACCTATTGTGCAAAATACCTATAGAGAAAGGACTAAATAAATCTTGAACGAACT 735
DB 676 TATAGTAACCTATTGTGCAAAATACCTATAGAGAAAGGACTAAATAAATCTTGAACGAACT 735
QY 601 TATACGAAACATTTGTTGGACACATACAACTCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
DB 601 TATACGAAACATTTGTTGGACACATACAACTCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
QY 736 AATATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTTACTGTATTAGAT 795
DB 736 AATATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTTACTGTATTAGAT 795
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DB 661 ACTCGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTTAAACACTTACTGTATTAGAT 720
QY 796 ACTATCGCTCAATTTCTTTTATGATATAGATATAAGAGATA 833
DB 796 ACTATCGCTCAATTTCTTTTATGATATAGATATAAGAGATA 833
QY 721 ATCGTTGCTCTTTTCCGAACCTACGATGTTAGAACATA 758
DB 721 ATCGTTGCTCTTTTCCGAACCTACGATGTTAGAACATA 758

RESULT 15
PCT-US95-05431-26
; Sequence 26, Application PC/TUS9505431
; GENERAL INFORMATION:
; APPLICANT:
; STREET ADDRESS: 5501 Oberlin Drive
; APPLICANT: City: San Diego
; APPLICANT: State/Province: California
; APPLICANT: Country: US
; APPLICANT: Postal code/zip: 92121
; APPLICANT: Phone number: (619) 453-8030 Fax number: (619) 453-6991
; APPLICANT: Telex number:
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; TITLE OF INVENTION: Pseudomonas fluorescens
; NUMBER OF SEQUENCES: 34

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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05431
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-05431-26

Query Match 3.8%; Score 79.6; DB 6; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

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QY 388 ATTCGATTGCTTAATACAGACGCGCTTTAATAACAGCAATAAATAATTTTACACTTACA 447
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QY 496 ACTTATAAAACGCTATTACTACCTATTATGCGCAAGCTGCTAAATTTTCAATTTAAATTTA 555
DB 496 ACTTATAAAACGCTATTACTACCTATTATGCGCAAGCTGCTAAATTTTCAATTTAAATTTA 555
QY 448 AGTTTGAATCCCTCTTTTATCGGCTCTATGTTCAAGCGCGAATTTTACATTTACACTA 507
DB 448 AGTTTGAATCCCTCTTTTATCGGCTCTATGTTCAAGCGCGAATTTTACATTTACACTA 507
QY 556 TTACAAACAGGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCTTCCACAAAT 615
DB 556 TTACAAACAGGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCTTCCACAAAT 615
QY 508 TTAAGAGACGCTGATCGTTTGGCGAGGTTGGGACCTGGATATAGCTACTGTTAATAAT 567
DB 508 TTAAGAGACGCTGATCGTTTGGCGAGGTTGGGACCTGGATATAGCTACTGTTAATAAT 567
QY 616 GAACCTAATGCTGGAAACATCAGATGCTATTATAAACTTTTAAAGAAATATACCTAA 675
DB 616 GAACCTAATGCTGGAAACATCAGATGCTATTATAAACTTTTAAAGAAATATACCTAA 675
QY 568 C-----ATTATAATAGATTAAATAAATCTTATTCATAGA 600
DB 568 C-----ATTATAATAGATTAAATAAATCTTATTCATAGA 600
QY 676 TATAGTAACCTATTGTGCAAAATACCTATAGAGAAAGGACTAAATAAATCTTGAACGAACT 735
DB 676 TATAGTAACCTATTGTGCAAAATACCTATAGAGAAAGGACTAAATAAATCTTGAACGAACT 735
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DB 736 AATATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTTACTGTATTAGAT 795
QY 661 ACTCGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTTAAACACTTACTGTATTAGAT 720
DB 661 ACTCGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTTAAACACTTACTGTATTAGAT 720
QY 796 ACTATCGCTCAATTTCTTTTATGATATAGATATAAGAGATA 833
DB 796 ACTATCGCTCAATTTCTTTTATGATATAAGAGATA 833
QY 721 ATCGTTGCTCTTTTCCGAACCTACGATGTTAGAACATA 758
DB 721 ATCGTTGCTCTTTTCCGAACCTACGATGTTAGAACATA 758

Search completed: February 15, 2006, 03:31:12
Job time : 384 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 00:28:19 ; Search time 1543 Seconds
(without alignments)
11174.111 Million cell updates/sec

Title: US-10-782-570-3
Perfect score: 2085
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2085	100.0	2085	8	US-10-782-570-3
2	2085	100.0	2235	8	US-10-782-570-1
3	1794.4	86.1	2208	8	US-10-783-417-1
4	161.2	7.7	4896	6	US-09-756-526A-3
5	161.2	7.7	4896	6	US-10-345-020-3
6	161.2	7.7	4896	6	US-10-342-821-3
c 7	117	5.6	15548	6	US-10-311-455-2128
8	100.6	4.8	3684	9	US-10-929-754-2
c 9	99.2	4.8	3673778	6	US-10-312-841-1
c 10	93.6	4.5	8056	8	US-10-473-126-386
c 11	86.8	4.2	8056	8	US-10-473-126-240
12	83.2	4.0	8056	8	US-10-473-126-386
13	79.6	3.8	3522	3	US-09-826-660-5
14	79.6	3.8	3522	3	US-09-837-961-7
15	79.6	3.8	3522	8	US-10-825-751-7
16	77.8	3.7	3504	5	US-10-089-678-2
17	77.8	3.7	3690	5	US-10-089-678-3
18	77.2	3.7	1959	7	US-10-614-076-13
c 19	77	3.7	18154	6	US-10-311-455-227
20	76.4	3.7	8056	8	US-10-473-126-240
21	75.6	3.6	1482	7	US-10-614-076-69
22	75.6	3.6	1956	7	US-10-614-076-51
23	75.6	3.6	1956	7	US-10-614-076-55

24	75.6	3.6	1956	7	US-10-614-076-57
25	75.6	3.6	1959	5	US-10-232-665-1
26	75.6	3.6	1959	7	US-10-614-076-1
27	75.6	3.6	1959	7	US-10-614-076-15
28	75.6	3.6	1959	7	US-10-614-076-17
29	75.6	3.6	1959	7	US-10-614-076-19
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36	75.6	3.6	1959	7	US-10-614-076-37
37	75.6	3.6	1959	7	US-10-614-076-41
38	75.6	3.6	1959	7	US-10-614-076-43
39	75.6	3.6	1959	7	US-10-614-076-45
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41	75.6	3.6	1959	7	US-10-614-076-65
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43	75.6	3.6	1959	7	US-10-614-076-97
44	75.6	3.6	2280	7	US-10-614-076-102
c 45	75	3.6	5930	6	US-10-311-455-490

ALIGNMENTS

RESULT 1
US-10-782-570-3
; Sequence 3, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2085
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2085)
US-10-782-570-3

Query Match	100.0%;	Score 2085;	DB 8;	Length 2085;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2085;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	ATGTGTCGAAGGAATACAAATATGGTGAATAATTCGAGACATTTGCTAGTGTGATACA	60	
Db	1	ATGTGTCGAAGGAATACAAATATGGTGAATAATTCGAGACATTTGCTAGTGTGATACA	60	
Qy	61	ATTGCTCAGTTAGTGCAGGTACTTGTATCCGGTACTCTGTTAGCCGGTATAGGTGGG	120	
Db	61	ATTGCTCAGTTAGTGCAGGTACTTGTATCCGGTACTCTGTTAGCCGGTATAGGTGGG	120	
Qy	121	CTCACTTCTATATCCGACCGATAGGATAATAGTGTCTATAATAATATCTTTTGGTACC	180	
Db	121	CTCACTTCTATATCCGACCGATAGGATAATAGTGTCTATAATAATATCTTTTGGTACC	180	
Qy	181	CTAATCACTGTCTTTTGGCCCGGGGAACAAGACAAAACAGTATGACACAAATTATT	240	

181 CTAATCACTGCTCTTTGGCCGGGAGAACAGACAAAACAGATATGGACACAATTTAT 240
182
241 AAAATCGGAGAAATTTTGTGATACACCGTTAAACAGAAAGCATAAAAACAGCTAAAGTTA 300
242
241 AAAATCGGAGAAATTTTGTGATACACCGTTAAACAGAAAGCATAAAAACAGCTAAAGTTA 300
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301 CAACTTTAGAGGATTTAGACAAATTTACAAGCTATTAATACAGCATTAGATGATGG 360
302
301 CAACTTTAGAGGATTTAGACAAATTTACAAGCTATTAATACAGCATTAGATGATGG 360
303
361 AGAAATTTAAAGACTACAAGCTCTGATTAACCAACCATCATCAGCATTTACAACAAGCT 420
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363
421 GCCTTGACTCTTAAAAATACGAATTTGAGAAATGTTTACAATGATTTTATTCGAGAAATACCT 480
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541 TTTTCATTTAAATTTATTAACAACAGGTGCTGAATTCGCTGATGAATGGAATGCAGATATA 600
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601 CATCTTCAAAATTTGAACCTTAATGCTGGAACATCAGATGACTATTATTAATCTTTTAAAA 660
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661 GAAATATACCTTAATATAGTAACTATTGTCGAAATACCTATAGAGAAAGCTAATAATA 720
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1081 GCTACGACAGGAACCTGAAATTTATATGAGAGAAAGAACAGGTCACCCCAACAAAACCT 1140
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1201 TCCCTTTTCTTAACATATACCTTACAAATTAATCAAAATGGAATTTATTAATAATATCA 1260
1203
1261 CTTAGTAATAATTAACATATTCAGCTGGGGGGAATTTATCTAATGATATAAAGAAACAACT 1320
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1321 GATTTTCAATTTCTCTGTAAAAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCA 1380
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1321 GATTTTCAATTTCTCTGTAAAAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCA 1380
1323
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1382
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1383
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1443
1501 AATAGAAATATGCAATATCAGATAAAATTAATCAATGATCCAGCAATCAAGGTAAC 1560
1502
1501 AATAGAAATATGCAATATCAGATAAAATTAATCAATGATCCAGCAATCAAGGTAAC 1560
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1681 TATTTACATTTAGACTTCGATACGCTACAAATGGTCTGGAAATACCTCTTCTTAATATATCT 1740
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1863
1921 ATTTTAACTCATTTGATAAAATGAATTTATACCAATTTACTTCTGTACGCCAAATATAGA 1980
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1981 GAAAAACAAAATTTAGAAAATCTATCCAAACAAAATTAATAATATTTTCAAAATCATACA 2040
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RESULT 2

US-10-782-570-1
; Sequence 1, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; PRIOR FILING DATE: 2004-02-19
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 1
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2235)
US-10-782-570-1

Query Match      100.0%; Score 2085; DB 8; Length 2235;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2085; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 151 ATGTGTCAGGGAATACACAAATATGTTGATTAATTTTCGAGACATTTCTAGTGTGTATACA 210
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Db 211 ATTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTGTAGCCGGTATAGGTGG 270
Qy 121 CTCACCTTCTATATCCGACCGATAGGAATAATAGGTGCTATATAATATCTTTTGTGACC 180
Db 271 CTCACCTTCTATATCCGACCGATAGGAATAATAGGTGCTATATAATATCTTTTGTGACC 330
Qy 181 CTAATCACTGCTTTTGGCCCGGGAGAAACAAGACAAACAGTATGGACACAATTTATT 240
Db 331 CTAATCACTGCTTTTGGCCCGGGAGAAACAAGACAAACAGTATGGACACAATTTATT 390
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Db 391 AANAATGGGAGAAATTTTGTGTATACACCGTTAACGAAAGACATAAAACAGCTAAAGTTA 450
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Db 451 CAAACTTTAGAGGATTTAGACAAATATTAACAAGCTATTAATACAGCATTTAGATGG 510
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Qy 600 TTTTCATTTAAATTTATTACAAAGGCTGCTGAATTTGGCTGATGATGGAATGCGAGATATA 660
Db 750 TTTTCATTTAAATTTATTACAAAGGCTGCTGAATTTGGCTGATGATGGAATGCGAGATATA 710
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Qy 900 TCAATAGGAAGATAGGTGGCAATTAAGAACTGAACTTACAAGAGAAATTTTATACAACCTGAA 1050
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Db 1051 ATAAATTTTGACCGTCTTACTTACCTTGAAATTCACCAATCTCGCTATATGGAATAT 1110
Qy 961 AATTTAAACAGCTTCAGGCTTAGATTTATTTTCAATTTTATAGATGAACCTTATTTATACA 1020
Db 1111 AATTTAAACAGCTTCAGGCTTAGATTTATTTTCAATTTTATAGATGAACCTTATTTATACA 1170
Qy 1021 AAAAATGAAACGTAACGGGAATCGTTTAGTTGGTATTTCGGAATCGTAAATAGATCTACTTAT 1080
Db 1171 AAAAATGAAACGTAACGGGAATCGTTTAGTTGGTATTTCGGAATCGTAAATAGATCTACTTAT 1230
Qy 1081 GCTACGACAGGAACCTGAAATTTATATGGAAGAAAGAACAGGTCCACCCCAACAAAACCT 1140
Db 1231 GCTACGACAGGAACCTGAAATTTATATGGAAGAAAGAACAGGTCCACCCCAACAAAACCT 1290
Qy 1141 TTAATACCAATTTGAATCTTATAAAGTTTCAATTTGTAACCTGATAGCAAGTAACTCTCTACT 1200
Db 1291 TTAATACCAATTTGAATCTTATAAAGTTTCAATTTGTAACCTGATAGCAAGTAACTCTCTACT 1350
Qy 1201 TCCCTCTTTTCTTAAACATATCTTACAAATTAATCAAATTTGAACTTTTATTTAAATTAATCA 1260
Db 1351 TCCCTCTTTTCTTAAACATATCTTACAAATTAATCAAATTTGAACTTTTATTTAAATTAATCA 1410
Qy 1261 CCTAGTAATAAATAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATATAAATAAATCA 1320
Db 1411 CCTAGTAATAAATAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATATAAATAAATCA 1470
Qy 1321 GATTTTCAATTTCTGTAAAAAAGAGCTGTAAACCAATTTAATCCAAATTCGTTTACCA 1380
Db 1471 GATTTTCAATTTCTGTAAAAAAGAGCTGTAAACCAATTTAATCCAAATTCGTTTACCA 1530
Qy 1381 AGCTTAATAAGTTATAGTCAATATTTTATCCAGTCTTTTCTTTTATTTAATTTATCTCTATAA 1440
Db 1531 AGCTTAATAAGTTATAGTCAATATTTTATCCAGTCTTTTCTTTTATTTAATTTATCTCTATAA 1500
Qy 1441 ATTGGATTTAGCGCTTAAATATATTTATACAGGTGCAATAGGATGGACACACAGTAGTGT 1500
Db 1591 ATTGGATTTAGCGCTTAAATATATTTATACAGGTGCAATAGGATGGACACACAGTAGTGT 1650
Qy 1501 AATAGAAATTAATGCAATATCAGATATAAATAATTTACAATGATCCCGCAATCAAAGGTAAAC 1560
Db 1651 AATAGAAATTAATGCAATATCAGATATAAATAATTTACAATGATCCCGCAATCAAAGGTAAAC 1710
Qy 1561 AGTCTTGATCAAACTCTAAGGTAAATTTGAAGGACCTGCTCATACAGGAGGAAACTTGGTT 1620
Db 1711 AGTCTTGATCAAACTCTAAGGTAAATTTGAAGGACCTGCTCATACAGGAGGAAACTTGGTT 1770
Qy 1621 TATTTACAAAGTCAAGGGCGTTTAGAGATTAATGATAGAACTCTCTAATTTCTACACAATCT 1680
Db 1771 TATTTACAAAGTCAAGGGCGTTTAGAGATTAATGATAGAACTCTCTAATTTCTACACAATCT 1830
Qy 1681 TATTTACATTTAGATTCGATACGCTACAAATTTGGTCTGGAATATCTCTCTCTAATATATCT 1740
Db 1831 TATTTACATTTAGATTCGATACGCTACAAATTTGGTCTGGAATATCTCTCTCTAATATATCT 1890
Qy 1741 CTTCACATACAGGAGTAATAGGAATACCCTCAACGACTCAACACACACTTTTCTCTGCT 1800
Db 1891 CTTCACATACAGGAGTAATAGGAATACCCTCAACGACTCAACACACACTTTTCTCTGCT 1950
Qy 1801 ACAATTTATATAATTTTACATACGAGATTTTGGGTATTTTCCAAATTTTCCAAAGTACAGTA 1860
Db 1951 ACAATTTATATAATTTTACATACGAGATTTTGGGTATTTTCCAAATTTTCCAAAGTACAGTA 2010
Qy 1861 ACATTTACTTTTAAATTCGAAACATACCAATTTATTTAATTCGTGAGATGATCAAAATCA 1920
Db 2011 ACATTTACTTTTAAATTCGAAACATACCAATTTATTTAATTCGTGAGATGATCAAAATCA 2070
Qy 1921 ATTTTAAATCATTTGATTAATTTGAAATTTATACCAATTTACTCTCTGTACGCCAAATAGA 1980
Db 2071 ATTTTAAATCATTTGATTAATTTGAAATTTATACCAATTTACTCTCTGTACGCCAAATAGA 2130
Qy 1981 GAAAAACAAAAATTTAGAACTTATCCAAACAAAAATATAATATATTTTTCACAAATCATACA 2040
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Db 2131 GAAAAACAAAATAGAACTCCAAACAAAATAAATACATTTTTCACAAATCATA 2190
Qy 2041 AAAAAATCTTTAAATATAGAAGCCACAACTATGATATTGATTA 2085
Db 2191 AAAAAATCTTTAAATATAGAAGCCACAACTATGATATTGATTA 2235

RESULT 3
US-10-783-417-1
; Sequence 1, Application US/10783417
; Publication No. US20040216186A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274146
; CURRENT APPLICATION NUMBER: US/10/783,417
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,806
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2208)
US-10-783-417-1

Query Match 86.1%; Score 1794.4; DB 8; Length 2208;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1908; Conservative 0; Mismatches 141; Indels 9; Gaps 2;

Qy 1 ATGTGTCAGGGGAATACAAATATGTGTGATAATTCGAGACATTTCTAGTGTCTGATACA 60
Db 154 ATGTGTCAGGGGAATACAAATATGTGTGATAATTCGAGACATTTCTAGTGTCTGATACA 213
Qy 61 ATGTGTCAGTTAGTCAGGTACTATTTGATCCGGTACTCTGTAGCCGGTATAGTGGG 120
Db 214 ATGTGTCAGTTAGTCAGGTACTATTTGATCCGGTACTCTGTAGCCGGTATAGTGGG 273
Qy 121 CTCACCTTCTATATCCGGCCGGATAGGAATAATAGGTGCTATAATAATATCTTTTGTACC 180
Db 274 CTCACCTTCTATATCCGGCCGGATAGGAATAATAGGTGCTATAATAATATCTTTTGTACC 333
Qy 181 CTAATCAGTCTTTTGGCCGGGAGAACAAAGACAAACAGTATGGACACAAATTTAT 240
Db 334 CTAATCAGTCTTTTGGCCGGGAGAACAAAGACAAACAGTATGGACACAAATTTAT 393
Qy 241 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACGAAAGCATAAAAAGCTTAAAGTTA 300
Db 394 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACGAAAGCATAAAAAGCTTAAAGTTA 453
Qy 301 CAAACTTTAGAGGATTTAGACAAATATTTACAAAGCTATAATACAGCATTAGATGTTGG 360
Db 454 CAAACTTTAGAGGATTTAGACAAATATTTACAAAGCTATAATACAGCATTAGATGTTGG 513
Qy 361 AGAAAAATTTAAAGACTTACAAGCTCTCGATTACCAACCATCATCAGCATTTACAAAGCT 420
Db 514 AGAAAAATTTAAAGACTTACAAGCTCTCGATTACCAACCATCATCAGCATTTACAAAGCT 573
Qy 421 GCCTTGACTCTTAAAAATACGAATTTGAGAATTTGACAATGATTTTATTCGAGAAATACCT 480
Db 574 GCCTTGACTCTTAAAAATACGAATTTGAGAATTTGACAATGATTTTATTCGAGAAATACCT 633
Qy 481 GGTTCCTCACTTGAACCTTATAAAACGCTATTACTACCTATTATTATGCGCAAGCTGCTAAT 540
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Db 634 GGTTCCTCACTTGAACCTTATAAAACGCTATTACTACCTATTATTATCGCAAGCTGCTAAT 693
Qy 541 TTTTCATTTAAATTTTATACAAACAAAGTGCTGAATTTGGCTGATGAATGGAATGAGATATA 600
Db 694 TTTTCATTTAAATTTTATACAAACAAAGTGCTGAATTTGGCTGATGAATGGAATGAGATATA 753
Qy 601 CATCCTTCACAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATATAACTTTTAAAA 660
Db 754 CATCCTTCACAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATATAACTTTTAAAA 813
Qy 661 GAAAAATATACCTTAAATATAGTAATCTATTGTGCAATACCTATAGAGAAAGGACTTAAATAA 720
Db 814 GAAAAATATACCTTAAATATAGTAATCTATTGTGCAATACCTATAGAGAAAGGACTTAAATAA 873
Qy 721 CTTGAAACGAAACCTTAATATGAGATGGAGTATATTATTAATGATTTATCGAAGATATATGACT 780
Db 874 CTTGAGAGCGAAACCAATATGAAATGGAGTATATTATTAATGACTATTCGAAGATATATGACC 933
Qy 781 ATTACTGTATTAGATACTATCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGAT 840
Db 934 ATTACTGTATTAGATACTATCGCTCAATTTCTTTTATGATATAAAGAGATATAGAGAT 993
Qy 841 TCAATAGGAAGAATAG-----GTGGCATTAAAACTGAACTTACAAAGAGAAAATTTATACA 894
Db 994 TCAATAGGAAGAATAGAAAGGCAATTAAGATGAACTCACAAGAGAAAATTTATACA 1053
Qy 895 ACTGAAATAAAATTTTGACCGTCTTACTTACCTTGAAATTCACCCCAATCTCGCTATAATG 954
Db 1054 ACTGAAATAAAATTTTGATGCTCTCTCTCAACTTAGAGTTCAACCCCAATCTAGCTACGATG 1113
Qy 955 GAATATTAATTTAAACAGTTTCAGGGCTTAGATTATTTTCAATTTTATGATGAACCTTATATT 1014
Db 1114 GAATATTAATTTAAACAGTTTCAGGGCTTAGATTATTTTCAATTTTATGAGCAATTTATTTT 1173
Qy 1015 TATACAAAAAATGAAACGTAACGGGAATCGTTAGTTGGTATTTCGCAATCGTAAATAGATCT 1074
Db 1174 TATACAGAAAATACAAATTCGGGAATCGTTAGTTGGTATTTCCTAATCGTATGACCT 1233
Qy 1075 ACTTATGCTACGACAGGAATGAAATTTATATGAGAGAAAGAACAGGTCCACCCACAACA 1134
Db 1234 ACTTATGCAATTAATTAACCTGAACTTTATATGAGAGAAAGAACAGGTTCACCCACAACA 1293
Qy 1135 AAAACCTTTAATACCAATTTGAATCCTATAAGTTTCAATTTGTAATCTGATAGACAACT 1194
Db 1294 AAAACAATAAGACCAATTTGAATCTTATAAGTTTCAATTTGTAATCTGATAGACAACT 1353
Qy 1195 CCTACTTCCCTTTTCTTAAACATACTTTTCAAAATTAATCAAAATGAACTTTATTTAAAT 1254
Db 1354 CCGTTTCCCTATTTC---AACCACACTTTAATTAATCAAAATGAACTTTATTTAAT 1410
Qy 1255 AATTCACCTAGTAATTAATTAACATATTACGCTGGGGGAAATTTATCTAATGATAAAAAA 1314
Db 1411 GGCCTCATCTAACACACACTCAAAATTTACGAGGAGGGTCTTTATCTAATTTATCAAAAC 1470
Qy 1315 ACACTGATTTTCAATTTCTGTAAAAAGAGCTGTAAACCAATTTATTTAATCCAAATTCCT 1374
Db 1471 ACACTTTTCTTCAATTTCTGTAAAAAGAGCTGCAATCTAGTTAATGATCCAGGTGT 1530
Qy 1375 TTACCAAGCTATAATAGTTATAGTCAATTTTATCCAGTTTCTTTTATTTAATTTATTC 1434
Db 1531 TCACCAAACTTTAATTAATAGTCAATTTTATCCCATTTTATCCATTTTATTTACTATTCC 1590
Qy 1435 TATAAAATTTGATTAGCGCTAAATATATATATACAGGTGCAATAGGATGGACACACAGT 1494
Db 1591 TATGTGATTGGATTACAGCTACAAATATTAGATACAGGTGTATTAGGATGGACACACAGT 1650
Qy 1495 AGTGTTAATAGAAAATTAATGCAATATCAGATAAAATTAATCAATGATGATCCAGCAATCAA 1554
Db 1651 AGTGTGTAGATATAATGCAATATCAGATAAAATTAATTAATGATGATCCAGCAATCAA 1710
Qy 1555 GGTAAACAGTCTTTGATACAACTCTAAGGTAATTTGAAGGACCTGGTTCATACAGAGGAAAC 1614
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Db 1711 GGTAAACATCTTGATACAAACTCTAAGTAAATTGAAGGACCTGGTCATACAGGAGAAAC 1770
Qy 1615 TTGGTTTATTACAAAGCTCAAGGCGTTTGAAGATTACATGTAGAACTCTCTAATCTTACA 1674
Db 1771 TTGGTTTATTACAAAGCTCAAGGCGTTTGAAGATTACATGTAGAACTCTCTAATCTTACA 1830
Qy 1675 CAATCTTATTACATAGACTCGATACGCTACAAATGGTGTGGAATATCTCTTCCTAAT 1734
Db 1831 CAATCTTATTCAATAGACTTCGATATGCTACAAATGGTGTGGAATATCTCTTCCTAAT 1890
Qy 1735 ATATCTCTTCAATACACAGGAGTAAATAGGAATACCACTCAACGACTCAACAACTTTT 1794
Db 1891 ATATCTCTTCAATACACAGGAGTAAATAGGAATACCACTCAACGACTCAACAACTTTT 1950
Qy 1795 TCTGGTCAAAATTAATAATTTACAATACGAGATTTTGGGTATTTTCCAAATTTCCAAAT 1854
Db 1951 TCTGGTCAAAATTAATAATTTACAATACGAGATTTTGGGTATTTTCCAAATTTCCAAAT 2010
Qy 1855 ACAGTACATTTACCTTTAAATCGAAACATACCAATTTATATTTAATCGTGAGATGTATCA 1914
Db 2011 ACAGTACATTTACCTTTAAATCGAAACATACCAATTTATATTTAATCGTGAGATGTATCA 2070
Qy 1915 AATTCAATTTTAAATCATTTGATAAAATTTGAATTTATACCAATTTCTCTCTGTACGCCAA 1974
Db 2071 AATTCAATTTTAAATCATTTGATAAAATTTGAATTTATACCAATTTCTCTCTGTACGCCAA 2130
Qy 1975 AATAGAGAAACAAAAATTTAGAACTATCCAAACAAAAATAAATAAATTTTCCAAAT 2034
Db 2131 AATAGAGAAACAAAAATTTAGAACTATCCAAACAAAAATAAATAAATTTTCCAAAT 2190
Qy 2035 CATACAAAAATACCTTTA 2052
Db 2191 CATACAAAAACACTTTGA 2208

RESULT 4
US-09-756-526A-3
; Sequence 3, Application US/09756526A
; Patent No. US20020038005A1
; GENERAL INFORMATION:
; APPLICANT: Jana, Wojciechowska
; APPLICANT: Evgeny, Lewitin
; APPLICANT: Ludmila, Revina
; APPLICANT: Igor, Zalunin
; APPLICANT: Galina, Chestukhina
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: S-30913A
; CURRENT APPLICATION NUMBER: US/09/756.526A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 60/175,158
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4896
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(4896)
; OTHER INFORMATION: Bacillus thuringiensis supsp. finitimus strain VKPM B-1161 (taxon
; OTHER INFORMATION: :29337
; NAME/KEY: CDS
; LOCATION: (1129)..(4458)
; OTHER INFORMATION: product: Cry28Aa1 delta-endotoxin
; PUBLICATION INFORMATION:
; AUTHORS: Wojciechowska, et al.
; TITLE: Two novel delta-endotoxin gene families cry26 and cry28 from Bacillus
; TITLE: thuringiensis ssp. finitimus
; JOURNAL: FEBS Lett.
; VOLUME: 453
; ISSUE: 12
; PAGES: 46-48

; DATE: 1999-06-18
; DATABASE ENTRY DATE: ---
US-09-756-526A-3
Query Match 7.7%; Score 161.2; DB 3; Length 4896;
Best Local Similarity 57.0%; Pred. No. 3.3e-19;
Matches 385; Conservative 0; Mismatches 243; Indels 48; Gaps 3;
Qy 153 AGCTGTATTAATATATCTTTTGGTACCCCTTAATACACTGTCTTTTGGCCCGGGGAGAAACA 212
Db 1293 AGGTGTGTACTTATATATCAATTTGGAACCTTGGCTCCCGTCTTTGGCTGATCAGAGGA 1352
Qy 213 AGA---CAAAACAGTATGACACAAATTTATTAATAATGGGAGAAATTTTGTGTGATACACC 269
Db 1353 AGATCCAAAAAATTTGGTCAAAATTTATGAACACGAGAGAACCTTTTAAATCAAAC 1412
Qy 270 GTTAAACAGAAAGCATAAAAAGCTAAAGTTTACAACTTTTAGAAGGATTTAGACAAATATT 329
Db 1413 AATTTCTACAGCTGTAAAAGAAATAGCATATTAGCTCATCTAAATGGTTTAAAGATGTATT 1472
Qy 330 ACAAAGCTATAATACAGCATTTAGATGATTCGAGAAATTTAAAGAGACTTACAAAGCTCTCTGG 389
Db 1473 AAGTACTATGAAGAGCATTTTAAATGATTCGAGAGAAATCCAAAGTCAATATCTGCAG 1532
Qy 390 ATTACCAACCATCATCAGCATTTACAAACAAAGCTGCCTTGACTCTTAAAAATACGATTTAGAA 449
Db 1533 ATTGGTATCAGA-----GATTTGAAAA 1556
Qy 450 TGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAATCTTATAAAACGCT 509
Db 1557 CGCTCAATTTCAATTTTGAAGCAATATGCCAACACTCCAACTTCCCGATGACACATT 1616
Qy 510 ATTACTACCTATTATTCGCGCAAGCTGCTAAATTTTCAATTTAAATTTTATACAAAGGTGC 569
Db 1617 ATTATTAAGTTGCTATACAGAAAGCTGCAAAATTTACATTTGAATTTTATACATCAAGGTGT 1676
Qy 570 TGAATTCGCTGATGAATGGAATGCAGATATACATACCTCTTCAAAATGGAACCTAATGCTGG 629
Db 1677 ACAATTCGCGATCAATGGAATGCAGATCAACACATTTCAACAT-----GTTGAA 1727
Qy 630 AACATCAGATGATTTATTAATTAATCTTTTAAAGAAAAATATACCTAAATATAGTAACTATTG 689
Db 1728 GTCATCAGGTACTTATTATGACGAGCTATTGGTATATATTTGAAAAAGTATATTAATATTG 1787
Qy 690 TGCAAAATACCTATAGAGAGGACTTAATAAATCTTGAACCGAACCTAATATGAGATGAG 749
Db 1788 CACCAAGACATACCATAAAGGATTGAATCACCTTTAAAGAAATCAGAAAAAATCAGATGGA 1847
Qy 750 TATATTTAATGATTATCGAAGATATATGACTTATTACTGTATTAGATACCTATCGCTCAATT 809
Db 1848 TGCTTATAACATATGTCGAGAAATGACCTTAATTTGTTATGATCTTGTGCGCAACTTT 1907
Qy 810 TTCTTTTATGATATA 825
Db 1908 TCCTTTTATGATATA 1923

RESULT 5
US-10-345-020-3
; Sequence 3, Application US/10345020
; Publication No. US20030150018A1
; GENERAL INFORMATION:
; APPLICANT: Jana, Wojciechowska
; APPLICANT: Evgeny, Lewitin
; APPLICANT: Ludmila, Revina
; APPLICANT: Igor, Zalunin
; APPLICANT: Galina, Chestukhina
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: S-30913B
; CURRENT APPLICATION NUMBER: US/10/345,020
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/175,158
; PRIOR FILING DATE: 2000-01-07

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/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 3
/ LENGTH: 4896
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis
/ FEATURE:
/ NAME/KEY: source
/ LOCATION: (1)..(4896)
/ OTHER INFORMATION: product: Cry28Aa1 delta-endotoxin
/ PUBLICATION INFORMATION:
/ AUTHORS: Wojciechowska, et al.
/ TITLE: Two novel delta-endotoxin gene families cry26 and cry28 from Bacillus
/ TITLE: thuringiensis spp. finitimus
/ JOURNAL: FEBS Lett.
/ VOLUME: 453
/ ISSUE: 12
/ PAGES: 46-48
/ DATE: 1999-06-18
/ US-10-345-020-3

Query Match          7.7%; Score 161.2; DB 6; Length 4896;
Best Local Similarity 57.0%; Pred. No. 3.3e-19;
Matches 395; Conservative 0; Mismatches 243; Indels 48; Gaps 3;

QY 153 AGGTGCTATAATAATATCTTTGGTACCCTAATACATGCTCTTTGGCCCGGGGAGAAC 212
DB 1293 AGGTGGTACTTATATCATTTTGGAACTTGGCTCCCGTCTTTGGCCTGATCCAGAGGA 1352
QY 213 AGA---CAAAACAGTAGTGACACAAATTTATTAATGGGAGAAATTTTGTGTACACAC 269
DB 1353 AGATCCAAAATAATTTTGGTCAAAATTTATGAACACGAGAAAGACCTTTTAAATCAAC 1412
QY 270 GTTAAACAGAAACATATAAAGCTTAAAGTTACAAACTTTTAGAAGGATTTTAGACAAATATT 329
DB 1413 AATTCTACAGCTGTAAAGAAATAGCATTAAGTCTATCTAATGGTTTAAAGATGATT 1472
QY 330 ACAAAAGCTATAATACAGCATTTAGATTTGGAGAAAAATTTAAAAAGACTACAAGCTCCTGG 389
DB 1473 AACGTACTATGAAGAGCAATTTAATGATTTGGAAGAGAAATCCAAGTGCAATACTGCTCAG 1532
QY 390 ATTACCAACCATCATCAGCAATTAACAACAGCTGCTTGAATCTCTTAAATAATAGGATTGAGAA 449
DB 1533 ATTTGATATCACAGA-----GATTTGAAAA-----GATTTGAAAA 1556
QY 450 TGTTCACAATGATTTTATTTCGAGAAATACTGGTTTCCAACTTTGAAACTTATAAAACGCT 509
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QY 810 TTCCTTTTATGATATA 825
DB 1908 TCCTTTTATGATATA 1923

RESULT 6
US-10-342-821-3
/ Sequence 3, Application US/10342821
/ Publication NO. US20030154510A1
/ GENERAL INFORMATION:
/ APPLICANT: Jana, Wojciechowska
/ APPLICANT: Evgeny, Lewitin
/ APPLICANT: Ludmila, Revina
/ APPLICANT: Igor, Zalunin
/ APPLICANT: Galina, Chestukhina
/ TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
/ FILE REFERENCE: S-30913C
/ CURRENT APPLICATION NUMBER: US/10/342,821
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/175,158
/ PRIOR FILING DATE: 2000-01-07
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 3
/ LENGTH: 4896
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis
/ FEATURE:
/ NAME/KEY: source
/ LOCATION: (1)..(4896)
/ OTHER INFORMATION: Bacillus thuringiensis supsp. finitimus strain VKPM B-1161 (taxon
/ OTHER INFORMATION: :29337
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1129)..(4458)
/ OTHER INFORMATION: product: Cry28Aa1 delta-endotoxin
/ PUBLICATION INFORMATION:
/ AUTHORS: Wojciechowska, et al.
/ TITLE: Two novel delta-endotoxin gene families cry26 and cry28 from Bacillus
/ TITLE: thuringiensis spp. finitimus
/ JOURNAL: FEBS Lett.
/ VOLUME: 453
/ ISSUE: 12
/ PAGES: 46-48
/ DATE: 1999-06-18
/ US-10-342-821-3

Query Match          7.7%; Score 161.2; DB 6; Length 4896;
Best Local Similarity 57.0%; Pred. No. 3.3e-19;
Matches 385; Conservative 0; Mismatches 243; Indels 48; Gaps 3;

QY 153 AGGTGCTATAATAATATCTTTTGGTACCCTAATACATGCTCTTTGGCCCGGGGAGAAC 212
DB 1293 AGGTGGTACTTATATCATTTTGGAACTTGGCTCCCGTCTTTGGCCTGATCCAGAGGA 1352
QY 213 AGA---CAAAACAGTAGTGACACAAATTTATTAATGGGAGAAATTTTGTGTGATACAC 269
DB 1353 AGATCCAAAATAATTTTGGTCAAAATTTATGAACACGAGAAAGACCTTTTAAATCAAC 1412
QY 270 GTTAAACAGAAACATATAAAGCTTAAAGTTACAAACTTTTAGAAGGATTTTAGACAAATATT 329
DB 1413 AATTCTACAGCTGTAAAGAAATAGCATTAAGTCTATCTAATGGTTTAAAGATGATT 1472
QY 330 ACAAAAGCTATAATACAGCATTTAGATTTGGAGAAAAATTTAAAAAGACTACAAGCTCCTGG 389
DB 1473 AACGTACTATGAAGAGCAATTTAATGATTTGGAAGAGAAATCCAAGTGCAATACTGCTCAG 1532
QY 390 ATTACCAACCATCATCAGCAATTAACAACAGCTGCTTGAATCTCTTAAATAATAGGATTGAGAA 449
DB 1533 ATTTGATATCACAGA-----GATTTGAAAA-----GATTTGAAAA 1556
QY 450 TGTTCACAATGATTTTATTTCGAGAAATACTGGTTTCCAACTTTGAAACTTATAAAACGCT 509
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Db 1557 CGCTCAATTTTGTAAAGCAATATGCCCAACTCCCACTTCCCAAGTATGACACTT 1616
Qy 510 ATTACTACCTATTATATGCGCAAGCTGCTAAATTTTCAATTTTAAATTTTATTACAAAGGTGC 569
Db 1617 ATTATTAAAGTTGCTATACAGCAAGCTGCAAAATTTTACATTTTGAATTTTATACATCAAGGTGT 1676
Qy 570 TGAATTTGGCTGATGGAATGGAATGAGATATACATCTTTCACAAATTTGAACTTAATGCTGG 629
Db 1677 ACAATTTGGCGATCAATGGAATGGAATGAGATCAACCAATTCACCAAT-----GTTGAA 1727
Qy 630 AACATCAGATGACTATTATATAAATTTTAAAGAAATATACCTTAAATATAGTAATG 689
Db 1728 GTCATCAGGTACTTATTATGAGAGCTTTGGTATATATTGAAAGTATATTATTTATG 1787
Qy 690 TGCAAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACTTAATATGAGATGGAG 749
Db 1788 CACCAAGACATACCATAAGGATTGAATCACTTAAAGAAATCAGAAATTCATGGGA 1847
Qy 750 TATATTTAATGATTTATCGAAGATATATGACTATTACTGTATTAGATACTATCGCTCAATT 809
Db 1848 TGCTTATAACACATATCGTCGAGAAATGACCTTAATTTGTTATGGATCTTGTGCAACTTT 1907
Qy 810 TTCTTTTATGATATA 825
Db 1908 TCCTTTTATGATATA 1923

RESULT 7
US-10-311-455-2128/c
; Sequence 2128, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; FILE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311.455
; PRIOR FILING DATE: 2002-12-16
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 2128
; LENGTH: 15548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2128

Query Match 5.6%; Score 117; DB 6; Length 15548;
Best Local Similarity 43.6%; Pred. No. 6.2e-11;
Matches 819; Conservative 0; Mismatches 1040; Indels 18; Gaps 6;

Qy 218 AAACAGTATGACACAAATTTTAAATGGGAGAAATTTTGTGATACACCGTTAACAG 277
Db 13398 ATAAATATACACGCATATAATATATATACGTATAAAATATATATAATATAATATACACGT 13339
Qy 278 AAGCATAAACAGCTAAAGTTACAACTTTTAGAAGGATTTAGACAAATATTACAAAGCT 337
Db 13338 CTAATATATATATATATAAAATTTTCAGTATAAAATATATATCTCAAATATATATAT 13279
Qy 338 ATAATACAGCATTAGATGATTTGGAGAAATTTAAAGAACTACAGCTCTCGGATTAACAC 397
Db 13278 AAATATATATCTAAATATATATATAAAATATATATCTAAATATATATATAATAAATA 13219
Qy 398 CATCATCAGCATTAACAAGCTGCTTGACTCTTAAATATGAGATTTGAGATGTTTCA 457
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Db 13218 TATATCTAAATATATATATAAAATATATATCTAAATATATATATAATAATATATATC 13159
Qy 458 ATGATTTTATTCGAGAAATACCTGGTTTCCAACCTTGAACCTTATAAAACGCTATTACTAC 517
Db 13158 TAAATATATATATATAATAAAATATATATCTAAATATATATATAATAATAATATATAA 13099
Qy 518 CTATTTATGCGCAAGCTGCTAAATTTTCAATTTTAAATTTTATTACAAAGGTGCTGAAATGG 577
Db 13098 ATATATATATATAA---AATATATAAAATATATATATAATAATATATATAATAAATA 13042
Qy 578 CTGATGAATGAATGAGATATACATCTTTCACAAATTTGAACCTTAATGCTTGGACATCAG 637
Db 13041 TACATATATAAAATATATATACATATACATATATAAAATACATATATAACAATAT-AT 12983
Qy 638 ATGACTATTATTAACCTTTTAAAGAAATATACCTTAATATAGTAATCTATTGTGCAATA 697
Db 12982 ATATAAAATATATATAAAATATATATAATAATATATATAATAATATATATATACGAATA 12923
Qy 698 CCTATAGAGAGGACTAAATATAAATTTTCGAAACGAACTTAATATGAGATGAGATATATTA 757
Db 12922 TATATATACGAATATATATATAATATATATACGAATATATATATACGAATATATATA 12863
Qy 758 ATGATTTATCGAAGATATATGACTATTACTGTATTAGATATCTATCGCTCAATTTTCTTTT 817
Db 12862 TAATATATATACGAATATATATATACGAATATATATAATAATATATATAATAATATATAT 12803
Qy 818 ATGATATAAGAGATACAAAGATTCATAGGAGAAATAGGTGGCATTTAAACTCGAACTTA 877
Db 12802 ACGAAATATATATACGAATATATATAATAATATATATAATAATATATATAATAACGAA 12743
Qy 878 CAAGAGAAATTTTATACAACTGAAATAAATTTTGACCGCTCTTACTTACCTTGAAATTTCAAC 937
Db 12742 TATATATATAATATATATAATAATAATATATAA-CGAAATATATATATATATATATAT 12684
Qy 938 CCAATCTCGCTTAATGGAATATAATTTAAACACGCTTCAGGCTTAGAATATATTTTCATTTT 997
Db 12683 AAAATATATATACGAATAAATATATAATATATAATAATAATAATAATAATAATAAATA 12624
Qy 998 TAGATGAACCT-TATATTTTATACAAAAAAGTAAACGCTACGGGAATCGTTTATGTTGGTATT 1056
Db 12623 TATATAATAATATATATAATAACATATATACATATAATAATATATATAATAATAATATACA 12564
Qy 1057 GCGAATCGTAATAGATCTACTTATGCTACGACAGCAACTGAAATTTATATATATATATAT 1116
Db 12563 TAAATATATATATAATAAATATATACATAAAATATATATAATAATAATAATAATAATAA 12504
Qy 1117 ACAGGTCACCCCAACAACAAACTTTA-----ATACCATTTGAATCTCTATAAGTTT 1167
Db 12503 ATATATATATAATAAATATATATACATAAAATATATATAATAATAATAATAATAATAA 12444
Qy 1168 TCAATTTGTAAGTATAGACAGTAACCTCTACTTTCCCTTTTCCCTAACATATATCTTTACA 1227
Db 12443 ATATATATAACATATATACATAAAATATATATAATAATAATAATAATAATAATAATA 12384
Qy 1228 ATTAATCAAAATTTGAACCTTTTATTTAAATAATTCACCTAGTAATAAATTAACATATT 1287
Db 12383 ATATAACATATATATATAATAACATATATATAATAACATATATATAATAACATATATAT 12324
Qy 1288 GGGGGGAATTTATCTAATGATATAAAAAACAACACTGAATTTTCAATTTTCCCTGTAATAA 1347
Db 12323 AACATATATATATAACATATATATAAACAATATATAATAACATATATATAATAATAACA 12264
Qy 1348 TGTAAACCAATTTAATTCAAATTTGTTTACCAAGCTATATAGTTTATAGTCATATTTTA 1407
Db 12263 TATATATAAACAATATATATAAACAATATATAAACAATATATAAACAATATATAAACAATA 12204
Qy 1408 TCCAGTTTTCTTTATTTAA---TTATTTCTTATAAAATTTGGATTAGCGCTAAATATATTA 1464
Db 12203 TATATAACATATATATAAACAATATATATAAACAATATATAAACAATATATAAACAATA 12144
Qy 1465 TATACAGGTGCAATAGGATGGACACACAGTAGTGTGTTAATAGAAATAATATGCAATATCAGAT 1524
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Db 12143 TATATATATACATATAAAAAATACATATAAAAAATACATATAAAAAATACATATAAAAA 12084
Qy 1525 AAAATAAATTACAAATGCCAGCAATCAAGAGGTAACAGCTTGTGATACAAACTCTTAAGGTA 1584
Db 12083 TAAACATATAAAAAATACATATAAAAAATACATATAAAAAATACATATAAAAAATACATATA 12024
Qy 1585 ATTGAAGGACCTGGTCATACAGGAGAACTTGGTTTATTTCACAAAGTCAAGGGCGTTTA 1644
Db 12023 AAAAAATANAATATATATAACATATAAAAAATANAATATATAACATATAAAAAATANAATA 11964
Qy 1645 GAGATTACATGTAGAACTCTTAATCTCACAACTCTTATTACATTAGACTTCGATACGCT 1704
Db 11963 TATATAACATATAAAAAATACATATAAAAAATANAATATAAAAAATANAATATAAAAAATA 11904
Qy 1705 ACAAAATGGTGGAAATACTCTTCTTAATATATCTTTCACATACACGAGAGTAATAGGA 1764
Db 11903 ATAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAA 11844
Qy 1765 ATACCACTCAAGACTCAACACACTTTTCTGGTACAAATATATAATTAATTAATTAACATAC 1824
Db 11843 TATAAAAAATANAATATAAAAAATANAATATAAAAAATANAATATAAAAAATATAAAAA 11784
Qy 1825 CGAGATTTTGGGTATTTCCAATTTCCAAGTACAGTAACATTACTTTAAATCGAAACATA 1884
Db 11783 TAAATATAAAAAATANAATATAAAAAATANAATATAAAAAATANAATATAAAAAATANAATAT 11724
Qy 1885 CCAATTATATTAAATCGTCAGATGATCAAAATTCAAATTTTAAATCAATGATTAATTAATTA 1944
Db 11723 AAAAAATAAAATATAAAAAATATAAAAAATANAATANAATATAAAAAATATAAAAAATANAATA 11664
Qy 1945 TTTATACCAATTAATCTCTCTGTACGCCAAATAGAGAAACAAAAATTAAGAACTATC 2004
Db 11663 AATATAAAAAATANAATATAAAAAATANAATATAAAAAATANAATATAAAAAATANAATA 11604
Qy 2005 CAAACAAAATAAATACATTTTTCACAAATCATACAAAAATACTTTAAATATAGAAAGCC 2064
Db 11603 ATATAAAAAATANAATATAAAAAATANAATANAATATAAAAAATANAATATAAAAAATANAATA 11544
Qy 2065 ACAAACTATGATTTGA 2081
Db 11543 ATAAATATAAAAAATAA 11527

RESULT 8
US-10-929-754-2
; Sequence 2, Application US/10929754
; Publication No. US20050124803A1
; GENERAL INFORMATION:
; APPLICANT: ABDULLAH, MODH AMIR
; TITLE OF INVENTION: INSECTICIDAL CRYSTAL PROTEINS WITH ENHANCED TOXICITY
; FILE REFERENCE: 22727/04179
; CURRENT APPLICATION NUMBER: US/10/929,754
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: 60/498,826
; PRIOR FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-929-754-2

Query Match 4.8%; Score 100.6; DB 9; Length 3684;
Best Local Similarity 48.6%; Pred. No. 3.5e-08;
Matches 705; Conservative 0; Mismatches 629; Indels 117; Gaps 11;
Qy 674 AATATAGTAACATTATGTGCAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAAC 733
Db 812 AATATATTGCATAGCAATTACATGATGATAAATAAAGGTTTAGATGTACTTTAGAAATAAAT 871
Qy 734 CTAAATATGAGATGGATATATTAAATGATTATCGAAGATATATGACTATTACTGTATTAG 793

Db 872 CTAAATGGCAATGGATTACGTTTAAATGATTATAAAGAGAGATGACTATTCAAGTATTAG 931
Qy 794 ATACTATCCCTCAATTTCTTTTATGATATATAAGAGATAC---AAAGATTCAATAGGAA 850
Db 932 ATATACTCGCTCTTTTGGCAGTTATGATCCACGTCGATACCCCTGCGGACAAAATAGATA 991
Qy 851 GAATAGGTGGCATTAAAATGAACTTACAAAGAGAAATTTATCAACTGAAATAAAATTTTG 910
Db 992 ATACGAAACTATCAAAAAACAGAAATTTTACAAGAGAGATTTTATACAGCTTTAGTAGAATCTC 1051
Qy 911 ACCGTCTTACTTACCTTGAAATTCACCCCAATCTCGCTTAATATGGAATATAATTTTAAACAC 970
Db 1052 CTTCTAGTAAATCTATAGCAGCCTGGAGGACGACTTACACGAGATGTTCAITTTATTC 1111
Qy 971 GTTCAGGGCTTAGATATATTTTCATTTTATAGATGAATTTATTTTATATACAAAATAAGAA 1030
Db 1112 CTTGGCTAAAGAGAGTAGATT-----TCTGGACCAATCTATATATCAAGATTTAAG 1163
Qy 1031 CGTACGGGNACTGTTTGTGTTTGGTATTCGAATCGTAATAGATCTACTTATGCTACGACAG 1090
Db 1164 APT-----TTTATCTGCCAATAAAATTTGGGTTTTCATATACAAATTTCTTCTGCAA 1213
Qy 1091 GAACTGAAATATATATGAGAGAAAGAACAGGTCCACCCCAACAAACAACTTTAATACCAT 1150
Db 1214 TGCAGAAAGTGGAAATTTATGGAAGTTCGT-----TTTGGTTCAA 1255
Qy 1151 TTGAATCCCTATAAAGTTTCAATTTGTAATGATAGACAAAGTAATCTCTACTTCCCTTTTC 1210
Db 1256 ATCTTACTCATCAAAATTCAACTTAATTTCTAAATGTTTATAAAACTTCTATACACAGATACTA 1315
Qy 1211 CTAAATATATCTTACAAATTAATCAAAATTTGAATTTTATTTAAATTAATTTACCTAGTAATA 1270
Db 1316 GCTCCCTCTTAATCGAGTTACAAAAATGGATTTCTACAAAATTTGAT----- 1362
Qy 1271 AATTAACATATTTCAGCTGGGGGAATTTATCTAAATGATAAAAAACAACTGATTTTCAAT 1330
Db 1363 -----GGTACTCTTGCTCTTATTAATTCAAATATAACACCACTCTGGAAGTTTAA 1414
Qy 1331 TTCTGTAAAAAAGACTGTAAACCAATTTAATTCACCAAAATTTGTACCAAGCTATAATA 1390
Db 1415 GGACCACATTTTGTGATTTTCAACAAATGAGAACACACCTAATCAACCAACTGTAAATG 1474
Qy 1391 GTTATAGTCATATTTATCCAGTTTCTTTTATTTAAATTTATTCCTATATAAAATTTGGATTAG 1450
Db 1475 ATTATACGCATATTTTAAGCTATAT-----AAAACTGATGTTA 1513
Qy 1451 CGCTAAATATATATATACAGGTGCATTAGGATGGACACACAGTAGTAGTTAATAGAAATA 1510
Db 1514 TAGATTATAACAGTAACAGGGTTTCATTTGCTTGGACACATAAGATTGTTGACCTTAATA 1573
Qy 1511 ATGCAATATCAGATAAAATAAATAAATGATATGATCCAGCAATCAAGGTAACAGTCTTGATA 1570
Db 1574 ATCAAAATATACACAGATGCTATACACAAAGTTCCGCGCGTAAATCTCAATCTCTTGAATG 1633
Qy 1571 CAACTCTAAGGTAATTAAGGACCTGCTCATACAGGAGGAACTTTGGTTTATTTTACAAA 1630
Db 1634 CAAACGCTAAAGTAATCAAGGGACCTGCTCATACAGGGGGGGATCTAGTTGCTCTTACAA 1693
Qy 1631 GTCA-----AGGCGCTTTAGAGATTATCATGTAGAAC-----TCCTAATTT 1669
Db 1694 GCATGGTACTCTATACAGGCAGCAATGGAGATTCAATGTAAACAAAGTATTTTAAATGATC 1753
Qy 1670 CTACAAATCTTTATTTACATTAGACTTCGATACGCTACAAATGGTGC---TGGNAATACTC 1726
Db 1754 CTACAAGAAGTTACGGATTTACGCATACGTTATGCTGCAATAGTCCAAATTTGTTGAATG 1813
Qy 1727 TTCCCTAATATATCTTCTTAAATACACAGGAGTAATAGGAATACCACCTCAACGACTCAACA 1786
Db 1814 TATCATATGATATCAAGGAGTTTCTAGAGGAACACAGATTAGTACAGAACTCTACGTTTT 1873
Qy 1787 ACACITTTTCTGGTACAAATTAATAATTTTACAATFACGAGATTTTGGGTA----- 1838

Db 1874 CAAGACCTAATAATAATACCTACAGATTTTAAATATGAAGAGTTTAGATACAAAGATC 1933
Qy 1839 -TTTCCAAATTCAGTACAGTAACTACCTTTAAATCGAAACATACCAATTTATATTTA 1997
Db 1934 CTTTGTGATGCAATTTGTACCGATGAGATTTATCTTAACTAACTGATAACTATAGCTATTC 1993
Qy 1898 ATCGTGCAGATGT--ATCAAAATTCAAATTTTAAATCATTTGATGATAAAATTTGAATTTTATACCA 1954
Db 1994 AACCAATTAACATGACTTCAATTAATCACTGATTTATGACAGATCGAAATTTATCCAA 2053
Qy 1955 TTACTTCTCTGTCAGCGCAAAATAGAGAAAACAAAAATTTAGAACTATCCAAACAAAA 2014
Db 2054 TCACTCAATCTGATTAGATGAGACAGAGAACCAAAATTTAGAACTCAGAACGAGAGTTG 2113
Qy 2015 TAAATACATTTTTCACAAATCATACAAAAATACCTTTAAATATAGAGCCACAACTATG 2074
Db 2114 TGAATGACCTGTTTACAAATGACGCGAAAGATGCAATTTAAACATTTGGAACGACAGATTATG 2173
Qy 2075 ATATTGATTAA 2085
Db 2174 ACATAGATCAA 2184

RESULT 9
US-10-312-841-1/c
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Query Match 4.8%; Score 99.2; DB 6; Length 3673778;
Best Local Similarity 43.7%; Pred. No. 9.6e-07;
Matches 811; Conservative 0; Mismatches 1028; Indels 15; Gaps 8;
Qy 218 AACAGTATGGACACAATTTTAAATGGGAGAAAATTTTGTGTGATACACCGTTAACAG 277
Db 1715486 ATAAATATATACATATAAAATATATATAATAAAATATACATATAAAATATATATAAAA 1715427
Qy 278 AACGATTAACAGCTAAAGTTACAACTTTAG-AGGATTTAGACAAATATTACAAAGC 336
Db 1715426 TATACATATAAAATATACATATAAAATATATATAAAATATACATATAAAATATATA 1715367
Qy 337 TATAATACAGCATTAGATGATTGGAGAAAATTTAAAGAGACTACAGCTCTCGGATTACCA 396
Db 1715366 TATAAATATACATATAAAATATATATAATAAAATATATAATAAAATATATATAAAA 1715307
Qy 397 CCATCATCAGCATTTACAAAGCTGCGCTTGACTCTTAAATATACGNTTTGAGAAATGTTCCAC 456
Db 1715306 ATATATATAAAATATATATAAAATATATATAATAAAATATATATAAAATATATAT 1715247
Qy 457 AATGATTTTATCGAGAAATACCTGGTTTCCAACTTTGAACTTATATAAAACGCTATTACTA 516
Db 1715246 ATAAATATATATAATAAAATATATATAATAAAATATATATAATAAAATATATAATAAA 1715187
Qy 517 CCTATTTATGGCA----AGCTGCTAAATTTTCATTTAAATTTTATTTACAAAGGCTGTA 572
Db 1715186 TATATATATAAAATATATATAATAAAATATATATAATAAAATATATATAATAAAATATA 1715127

Qy 573 ATTGGCTGATGAATGGAATGCAGATATACATCTTCCAAATTTGAACCTTAATCTCGAAC 632
Db 1715126 TATAAAATATATATAATAAAATATATATAATAAAATATATATAATAAAATATATATA 1715067
Qy 633 ATCAGATGACTATTATAAACTTTTAAAGAAATATACCTTAAATATAGTAGTAAGTATTGTGC 692
Db 1715066 TAAAAATATATATATAATAAAATATATATAATAAAATATATATAATAAAATATATATA 1715007
Qy 693 AAATACCTTAGAGAGAGGACTAAATAAACTTTCGAAACGAAACCTTAATATGAGATGGAGTAT 752
Db 1715006 AAATATATATATATAATAAAATATATATAATAAAATATATATAATAAAATATATA-TAT 1714948
Qy 753 ATTTAATGATTAATCGAAGATATATGACTATTACTGTATTAGATACACTACGCTCAATTTTC 812
Db 1714947 ACAAATATATATAATAAAATATATATAATAAAATATATATAATAAAATATATATAATAAA 1714888
Qy 813 TTTTATGATTAAGAGATACAAAGATTCAATAGGAAGATAGGTGGCACTTAAACTGA 872
Db 1714887 TATATATATAATAAAATATATAATAAAATATATACATATAAAATATATATACTATATATAAA 1714828
Qy 873 ACTTACAAGAGAAATTTATACAACTGAAATAAAATTTTGACCGTCTTACTTACCTTGAAT 932
Db 1714827 ATATAAATATATATAATAAAATATATATAATAAAATATATAATAAAATATATAATAAA 1714768
Qy 933 TCAACCCAAATCTCGTATATATGAATATAATTTAAACAGCTTCAGGGCTTAGATTTATTTTC 992
Db 1714767 TATACATATAAAATATATATAATAAAATATACATATAAAATATACATATAAAATATACA 1714708
Qy 993 ATTTTATGACTTATATATTTTATACAAAAATGAAACCTACGGGAATCGTTAGTTGG 1052
Db 1714707 TAAAAATATACATATAAAATATACATATAAAATATATATAAAATATATATA-TAAAAATATA 1714649
Qy 1053 TATTGCAATCGTAATAGATCTACTTATGCTAGCAGAGAACTGAAATTTATATATATATATAT 1112
Db 1714648 TATAAAATATATATATAATAAAATATATATAATAAAATATATATAATAAAATATACA 1714589
Qy 1113 AAGAACAGGTCCACCCCAACAAACAACTTTTAATACCAATTTGAATCTTATAAGTTTCAAT 1172
Db 1714588 TAAAAATATATATAATAAAATATATACATATAAAATATATAATAAAATATATAATAAAAT 1714529
Qy 1173 ---TGTAACGTAGACAAAGTAACTCTACTTCCCTTTTCCCTAACATATATCTTTACAT 1229
Db 1714528 ATATATAAAATATATATAATAAAATATATATAAAATATATAATAAAATATATAATAAA 1714469
Qy 1230 TAATCAATTTGAATTTTAAATTAATTCACCTAGTAATAAATAAATAAATTAATTCAGCTGG 1289
Db 1714468 TATAATAAAATATATAATAAAATATATATAATAAAATATATAATAAAATATATAATAAA 1714409
Qy 1290 GGGGAATTTATCTAATGATATAAAACAACTGATTTTCAATTTCTGTAAAAAAGACTG 1349
Db 1714408 ATATAAAATATATAATAAAATATATATAATAAAATATATAATAAAATATATAATAAA 1714349
Qy 1350 TAAACCAATTTAAATCCAAATTTGTTTACAGCTATAATAGTTTATAGTCATATTTTATC 1409
Db 1714348 TATATATAAAATATATAATAAAATATATA-TAAAAATATATAATAAAATATATAATAAA 1714290
Qy 1410 CCAGTTTCTTTATTTTAAATTTTCTTATAAAATTTAGGCTTAAATATATTTATATATAC 1469
Db 1714289 TATAAAATATATAATAAAATATATAAAATATATAAAATATATAATAAAATATATAAA 1714230
Qy 1470 AGGTGCATTTAGGATGGACACACAGTAGTGTTTAAATAGAAATTAATGCAATATCAGATAAAAT 1529
Db 1714229 TATATAATAAAATATATATAATAAAATATATAATAAAATATATAATAAAATATATAT 1714170
Qy 1530 AATTCAATGATCCAGCAATCAAAGGTAAACAGTCTTGATACAACTCTAAGGTAAATGA 1589
Db 1714169 AAAATATATATAATAAAATATATAATAAAATATATAATAAAATATATAATAAAATATA 1714110
Qy 1590 AGGACCTGGTCATACAGGAGGAAACTTGGTTTATTTTACAAAGTCAAGGCGCTTTAGAGAT 1649
Db 1714109 TAAATATATATAATAAAATATATATAATAAAATATATAATAAAATATATAATAAAATATAT 1714050
Qy 1650 TACATGTAGAACTCTTAATTTCTACACATCTTTATTTACATTAGACTTCGATTCAGCTA---C 1706

Db	1714049	AAAAATATATATAAAATATATATATAAAATATATATAAAATATATATAAAATATATATA	1713990
Qy	1707	AAATGGTGGTGGAAATCTCTTCTCTAAATATATCTTTACAAATACCAGGAGTAATAGGAAT	1766
Db	1713989	AAATATATATATAAAATATATAAAATATATATAAAATATATAAAATATATATAAT	1713930
Qy	1767	ACCACCTCAACGACTCAACAACACTTTTTCTCGTGACAAATTAATAAATTTACAATACGG	1826
Db	1713929	AAAAATATATAAAATATATATAAATATATAAATAATATATAAATATATAAATAATATAT	1713870
Qy	1827	AGATTTTGGGTATTTCCAAATTTCCAAAGTACAGTAACAATTTACCTTTAAATCGGAACATACC	1886
Db	1713869	ATATAAAATATATAAATATATATAAATAATATAAATAAATAATATATAAATAATATAAA	1713810
Qy	1887	ATTATATATTTAAATCGTGAGATGTATCAAAATTTCAATTTTAAATCATTCGATAAAATTCGAAT	1946
Db	1713809	ATATATATAAAATATATAAAATATATAAATAATATAAATAATATAAATAATATATAA	1713750
Qy	1947	TATACCAATTTACTCTCTCTGTCGCGCAAAATAGAGAAAAACAAAAATTTAGAACTATCCA	2006
Db	1713749	ATATATATATAAATATATATAAATATATAATTTATATATATATAAATATAAATAATATA	1713690
Qy	2007	AACAAAAATAAATACATTTTTCACAAATCATACAAAAAATACTTTAAATATAGA	2060
Db	1713689	TA-AAATATATATAAAATATATAAATAATATATAAATAATATATAAATAATATATA	1713637
RESULT 10			
US-10-473-126-386/c			
; Sequence 386, Application US/10473126			
; Publication No. US20040234973A1			
; GENERAL INFORMATION:			
; APPLICANT: Epigenomics AG			
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell			
; FILE REFERENCE:			
; CURRENT APPLICATION NUMBER: US/10/473,126			
; CURRENT FILING DATE: 2003-09-26			
; NUMBER OF SEQ ID NOS: 1258			
; SEQ ID NO 386			
; LENGTH: 8056			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)			
US-10-473-126-386			
Query Match 4.5%; Score 93.6; DB 8; Length 8056;			
Best Local Similarity 43.4%; Pred. No. 9e-07;			
Matches 847; Conservative 0; Mismatches 1079; Indels 26; Gaps 8;			
Qy	147	AATAATAGTGCTATATAATATCTTTTGGTACCTTAATCACCTGTCTTTGGCCCGCGG	206
Db	7433	AATAACATATATATATACATATTTTTTTTTTCCAAATATTTTTTTTTTAAAAATA	7374
Qy	207	AGAACAGACAAACAGTAGTAGGACACAATTTATTAATAATGGGAGAAATTTTTGTGTATAC	266
Db	7373	ATAAAAAAATAAAAAATTTATTTAAAAATTTTTTAAATAAAAAATTTAAAAATAAAAAA	7314
Qy	267	ACCGTTAACGAAAGCATAAACAGCTAAAGTTACAACTTTAGAGGATTTAGACAAAT	326
Db	7313	ATATTTTTTTTATATATCATATAAATAATATAAATAAATAAATAAATTTCAAAAAAATATAT	7254
Qy	327	ATTACAAAGCTATAATACAGCATTTAGATGTTGGAGAAATTTAAAGACTACAAGCTCC	386
Db	7253	ATTATATATTAATATTAATATTTTAAAAATAAATAAATATATATAAATAATTAATAA	7194
Qy	387	TGGATTACCAAC-CATCATCAGCATTTACAACAGCTCGCTTGACTCTTAAAAATACGATTTG	445
Db	7193	TTAATTTAAATCAAAACATAAATAAATAAATAAATAAATACATTTTACAAATTTATATAATA	7134
Qy	446	AGATGTTCCAAATGATTTTTTTCGGAAATATACCTGGTTCCAACTTGAACTTATAAAA	505

Db	7133	TTTTTATTAATATATTTAAAAAAATTTATAAAATTTATAAAATTTAAAAATTTAATTTAAAAA	7074
Qy	506	CGCTATTTACTACTCTATTTATGCGCAAGCTGTAAATTTTCATTTAAATTTTATTTACAACAAG	565
Db	7073	ATAATTTAAATTTTAAATTTTAAAAATTTTTTTTTTTTAAAAAATAACAAAAATAAT	7014
Qy	566	GTGCTGAATGGCTGATGAATGCAATGCGAGATATACATCTCTTCACAAATTTGAACC--TAA	623
Db	7013	ATTTTTTTTTTTTTTTTTTAAATTTAAAAATCAATATATTTTTTTATATATAAATCATATTTTAA	6954
Qy	624	TGCTGGAACATCAGATGACTATTATATAAATCTTTTAAAAAGAAAAATATACCTTAAAAATAGTAA	683
Db	6953	TAATAAAAAAATAAAAAATTTTAAAAAATAAATAAATTTCAATTTATTTCAAAAAAATAA	6894
Qy	684	CTATTGTGCAAAATCCTATPAGAGAGGACTAAATAAACTTCGAAAAAGAACCTTAATATGAG	743
Db	6893	AAAAATTAAACAAATTTTTTTTATAAAAAATTTTATTAATTTTCAATTTCAATTTATAAAAT	6834
Qy	744	ATGGAGTATTTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATCGC	803
Db	6833	TTTTTATTTATTTTTTTTAAAAAAATTTCAATTTCCAAATTTCAATTTATTTTATTTTTTTTA	6774
Qy	804	TCAAATTTTCTTTTATGATATAAGAGATACAAAAGATTTCAATAGGAGAAATAGGTGGCAT	863
Db	6773	TATTTTTTCAATTAATTTTTTAAATTTTAAATTTCAATTAATTTCAAAATTTATTTATTTTAA	6714
Qy	864	TAAAACTGAACTTACAAGAGAAA-----TTTATACAACCTGAAATAAATTTTGA	911
Db	6713	TCAACATTATAAAACATAAAAAAATTTTATTTTTTTTAAAAATTTTAAATTTAAAAATTTAAAA	6654
Qy	912	CGTCTTACTTACTTGTGAATTTCAACCCCAATCTCGTATATAATGGAATATAATTTTACACG	971
Db	6653	ATTTCATATAAAAAAATAAAAAATAAAAAATAAATAAATAAATAAATAAATAAATAAATAA	6594
Qy	972	TTTCAAGGCTTACATATATTTTCAATTTTATAGTCAACTTATATTTTATACAAAAAATGAAAC	1031
Db	6593	TTTTTTTTTCAATTTTAAATTTTAAATTAATAAATAAATAAATAAATAAATAAATAAATAA	6534
Qy	1032	GTACGGGAATCGTTAGTTGGTATTTCGGAATCGTAATAGATCTACTTATGCTACGACAGG	1091
Db	6533	ATTTTTCATACAAAATTTTACAAAAATTTTAAATAAACAATAAATAAATAAATAAATAATTTAT	6474
Qy	1092	AACTGGAATTTATATATGGAAGAAAGAACGGTCCACCACCAACAACAACTTTTAA--TACCA	1149
Db	6473	TATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	6414
Qy	1150	TTTGAATCCTATAAAAGTTTCAATTTGTAAGTATAGACAAGTAACCTCTACTTCCCTCTTT	1209
Db	6413	TATATATATAATATATAATATATAATTTTTTTTTTAAATAAATAAATAAATAAATAAATAA	6354
Qy	1210	CCTAACATATACTTTTCAATTAATCAAAATGAACCTTTTATTTAAATAAATTTTCACTAGTAAT	1269
Db	6353	ACACATTTTTTAAATATACATATAATACATTTTAAATTTTAAATTTTAAATTTTAAATAT	6294
Qy	1270	AAATTTAAATTTTACGCTGGGGGAA--TTTATCTAATGATAAATAAATAAATAAATAAATAA	1328
Db	6293	CATTTTTTTTTTATATTTTTTATTTTTTTTTTATTTTATTTTAAATTTTAAATTTTAAATTTAA	6234
Qy	1329	ATTTCTCTGTAAAAAAGACTGTAAACCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	1388
Db	6233	ACACATTTTATATATTAAATTTTAA	6174
Qy	1389	TAGTTATAGTCATATTTTATCCAGTTTTTCTTTATTTTAAATTTTCTCTATAAATAAT--TGGAT	1447
Db	6173	AAATTTTTTTTTTAAATTTTAAACAAACATTTTATAAATTTTAAATTTTAAATTTTAAATTTAA	6114
Qy	1448	TAGCGCTAAATATATATATACAGGTGCATTTAGGATGGACACACAGTAGTGTGTTAATAGMA	1507
Db	6113	AAACACATAAATACATTTTCAATATAAATAAATAAATTTTCAATTTTCAATTTTCAATTTTATTT	6054
Qy	1508	ATAATGCAATATCAGATAAATAAATAAATAAATTTTCAATGATCCAGCAATTTCAAGGTGTAACAGTCTTG	1567

Db 6053 ATAAATAA ---AAATACAAATTTATTAATATATATTTATACAAAAAATAATAAAAAA 5998
Qy 1568 ATACAAACTCTAAGGTAATGAAGGACCTGGTCATACAGAGGAAACITGGTTTATTAC 1627
Db 5997 AAAAAAATTTAAAAAATAAATAAAAAAATAAATAAACAACATATTAATTTATACAA 5938
Qy 1628 AAGTCAGGGCGTTAGAGATTACATGTAGAACTCCTAATTTCTACACAATCTTATACA 1687
Db 5937 TTTTATTTTATTTATTTATTTTAAATTTAAATTTAAATTTCAATTTCAATTTAAATTTT 5878
Qy 1688 TTAGACTTCGATACGCTACAAATGGTGGAAATACCTCTCTCTAATAATCTCTTACAA 1747
Db 5877 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 5821
Qy 1748 TACGAGAGTAATAGGAATACACCTCAAGGACTCAACAACCTTTTCTGGTACAAAT 1807
Db 5820 TAAAAACATAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 5761
Qy 1808 ATAAATTTTACAAATACGGAGATTTTGGGTATTTTCCAAATTTCCAACTACAGTAACAATTAC 1867
Db 5760 TTATAATACAAAAATTTAAACAATTTAAACAATTTTCAATTTATTTATTTATTTATTT 5701
Qy 1868 CTTTAAATCGAAACATACCATTTATATTTAATCGTCAGATGATCAAAATTTCAATTTAA 1927
Db 5700 CATCAATTTCAATCATTTTAAATTTTATTTTATTTTCAAAAAAATAAAAAATTTTAA 5641
Qy 1928 TCATTCATAAAAATTTATACCAATTTATCTCTCTCTGTACCCCAAAATAGAGAAAAAC 1987
Db 5640 AATTTAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 5581
Qy 1988 AAAAAATAGAACTATCCAAACAAATAAATAACATTTTTCACAAATCATACAAAAATA 2047
Db 5580 AATTTTATTTAATTTCAATTAATAATTTTAAATAAAAAAATAAAAAAATAAAAAAATA 5521
Qy 2048 CTTTAAATATAGAGCCACAAACTATGATATT 2079
Db 5520 AATTTAAATAAAAAATCAACAATAAATTT 5489

RESULT 11
US-10-473-126-240/c
; Sequence 240, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 240
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-240

Query Match 4.28; Score 86.8; DB 8; Length 8056;
Best Local Similarity 43.34; Pred. No. 1.6e-05;
Matches 727; Conservative 0; Mismatches 932; Indels 21; Gaps 6;
Qy 390 ATTACCAACCATCATCAGCATTTACAAACAGCTGCCTTGACTCTTTAAAAATACGATTTGAGAA 449
Db 1700 ATTTTATATTTTAAATAAATAAATTTTATCGTATTAATTAATAAATAAATTTTAA 1641
Qy 450 TGTTCAAAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAAACGCT 509
Db 1640 TTTTACGATTCGTTTATTTCCGATTTTAAATAATTAATAATTTATAAATAAATAAAT 1581
Qy 510 ATTACTACCTATTATGCGCAAGCTGCTAATTTTCAATTTAAATTTATTTACAAACAGTGC 569

Db 1580 ATTAATTTTAAATATAAATTTTAAAAAATAAATTTTATTTAAAAAATTTTAAAAACGTAT 1521
Qy 570 TCAATTTGGCTGATGAATGGAATGCAGATATACATCCTTCACAAATTTGAACCTAAATGCTCG 629
Db 1520 TTATATTTTATTTATTAATAATTAATTTTA-ATAATTAATTTATTTTATATATATTTTAT 1462
Qy 630 AACATCAGATGACTATTATAAACTTTTAAAGAAATATACCTAAATATAGTAACTATTGG 689
Db 1461 TAAAAAATAAATTTTATTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 1402
Qy 690 TCAAAATACCTATAGAGAGGACTAAATAAACTTCGAACGACCTAAATATAGATGGAG 749
Db 1401 CGATATTTATTTTATAAAAAAATAAATTTTAAATAAATAAATAAATAAATAAATTT 1342
Qy 750 TATATTTAATGATTTATCGAAGATATATGACTATTACTGTATTAGATACCTATCGCTCAAT 809
Db 1341 TTTTATTAATAATTTATTAATAATTTTATTAATTTTATTAATTTTAAAAAATAATACGT 1282
Qy 810 TTTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAAATAGGTGGCAATTAAAC 869
Db 1281 TTTTATATATTAATAATTAATTAATTTTAAAAATTTTAAAAAATAAATTAATAAATCG 1222
Qy 870 TGAACCTTCAAGAGAAATTTATACACTGAAATAAATTTTGACCGCTTACTTTACCTTGA 929
Db 1221 TAAAAAATAAATTTAAATTAATAATTTAAAAATTTTAAAAAATAAATTAATAAATCG 1162
Qy 930 AATTCACCACTCTCGCTATTAATGGAATATAATTTTAAACACGTTCAAGGCTTATAGATT 989
Db 1161 TATTAATTTTAAATTTTCGAATATCGAAAAAATAATTTAAAAACGAAATATATACGTTT 1102
Qy 990 TTTCAATTTTAGATGAATTTATATTTTATACAAAAATGAAACGTCAGGGAATCGTTAGT 1049
Db 1101 ABAACGTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1042
Qy 1050 TGGTATTCGAATTCGTAATAGATCTACTTATGCTACGACGAGGAACTGAAATTTAT 1108
Db 1041 GAAATTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 982
Qy 1109 GAGAAAGACAGCTCCACCCACCAACAAAACTTTAATACCATTTGAATTCCTATAAAGTTT 1168
Db 981 TATTTTATTCGTTTAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 922
Qy 1169 CAATTCGTAATGATAGACAAAGTAACCTCTACTTCC-----CCTTTTCTTAACTATAC 1223
Db 921 ACACGAAATATTAATAATATAAATTTTAAATAATTAACGAAATTTTATACGTAATAA 862
Qy 1224 TACAATTAATCAAAATTTGAATTTTATTTAAATAATTTCACTAGTAATAAATAATTA 1283
Db 861 AATAAAAAAATCGATTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAAT 802
Qy 1284 AGCTGGGGGGAATTTATCTAATGATAAAAAACAACCTGATTTTCAATTTCTCTGTAATA 1343
Db 801 TAAATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 742
Qy 1344 AGACTGTAAACCAATTTAATCCAAATTTGTTTAAAGCTATAAATAGTTATAGTCAAT 1403
Db 741 ATTATAATAAATTTTAAATTTTAAATTTTAAATAAATAAATAAATAAATAAATAA 682
Qy 1404 TTTATCCAGTTTCTTTTATTTTAAATTTTCTCTATAAATAAATTTGGATT-----AGC 1451
Db 681 TATTTTATTTTATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 622
Qy 1452 GCTAAATATATTATACAGCTGCATTTAGGATGCACACAGTAGTGTAAATAGAAATAA 1511
Db 621 TTTTATAATAATTTTATTAATAATTTTATTAATAATAAATAAATAAATAAATAAATA 562
Qy 1512 TGAATATCAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1571
Db 561 TATAATA-ATTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 503
Qy 1572 AAACCTTAAGGTAATTTGAAGGACCTGGTCAATACAGGAGGAACTTGGTTTATTTACAAG 1631
Db 502 AAATTTTAAATTTTATTTTAAATAATAAATAAATAAATAAATAAATAAATAAATAAATA 443

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QY 1632 TCAGGGCGTTAGAGATTACATGTAGAACTCCTAAATCTACACAATCTTATTACATTAG 1691
Db 442 TTTTAAAAAATAAATAAATTAATTAATAATTAATTAATAATTTTAAATTTATAAA 383
QY 1692 ACTTCGATACGCTACAAATGGTCTCGAAATACCTCTTCTTAATATATCTCTTACAATACC 1751
Db 382 TATTTTATTCGTTTTTTTTTTTTTTTAAATATATATATTTTTTATTTTATTTTAAAT 323
QY 1752 AGGAGTAATAGGAATACCCTCAACGACTCAACACATCTTTTCTGGTACAAATPATAA 1811
Db 322 ATTTTTTAAAAAATAATTTTAAAAAATAAATAAATTTTTTTTTTATAAATAAATTTAA 263
QY 1812 TAA-TTTACATACGAGATTTTGGGTATTTCCAAATTTCCAAGTACAGTAACATACCTT 1870
Db 262 AATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATATTTTTTAAAAATTTATAATAAT 203
QY 1871 TAAATCGAAACATACCAATTTATATTTAAATCGTCAGATGTATCAAAATTCAAATTTTAATCA 1930
Db 202 AATTAATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 143
QY 1931 TTGATAAAAATGTAATTTATACCAATTTACTTCTCTGTAGCCCAAAATAGAGAAAAACAAA 1990
Db 142 AAAAAAATATAAAAAATTAATAATAATAATTAATAATAATAAATAAATAAATAAATAAATA 83
QY 1991 AATTAGAACTATCCAAACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2050
Db 82 AATTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 23

RESULT 12
US-10-473-126-386
; Sequence 386, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

Query Match 4.0%; Score 83.2; DB 8; Length 8056;
Best Local Similarity 43.5%; Pred. No. 7.2e-05;
Matches 783; Conservative 0; Mismatches 993; Indels 24; Gaps 8;

QY 279 AAGCATAAACAGCTAAAGTTACAAACTTTAGAGAGATTTAGACAAATATTACAAAGCTA 338
Db 327 AATAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 386
QY 339 TAATACAGCATTAGATGATTGGAGAAAATTAAGAGACTACAGCTCCCTGGATTACCACC 398
Db 387 TAATTTAAAAATTAATTTAATAATATATTTTAAATATTTTATTTTATTTTAAAAATAT 446
QY 399 ATCATCAGCATTTACACAGCTCGCTTGACTCTTAAAAATACGATTTTGAAATGTTTCACAA 458
Db 447 AAAAAAATAATTAATTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 506
QY 459 TGAATTTTTCAGAAATACCTGGTTCCAACTTGAACCTTATAAAGCTATTACTACC 518
Db 507 TATTTTATAATATAAATATATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 562
QY 519 TATTTATGCCAGCTGCCTAAATTTTCAATTTAAATTTATTTACAAAGGTCGAATGGC 578
Db 563 ATGTTTTTAAAAATTTATTTATTTAATAATAATAATAATAATAATAATAATAATAATAATA 622
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QY 579 TGATGAATGGAATGCAGATATACATCCTTCACAAATTTGAACCTAATGCTGGAAACATCAGA 638
Db 623 TTTAAAAATTTTAAAAATAAATTTTAAATATAAATTTTAAATAAATAAATAAATAAATAA 682
QY 639 TGACTATTATATAAATCTTTTAAAAAGAAAAATATACCTAAAATATAGTAACTATTGTGCAATAC 698
Db 683 TAAATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 742
QY 699 CTATAGAGAGGACTTAAATATAAATCTTCGAAACGAACCTAATATGAGATGGAGATATATTAA 758
Db 743 AAAATTTTAAATTTTAAAAATTTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAA 802
QY 759 TGAATATCGAAGATATATGACTATTACTGTATAGATCTACTCGCTCAATTTTCTTTTATA 818
Db 803 AATAAATTTTATAAATGATTTTATAAATAAATTTTATAAATAAATAAATAAATAAATAAATA 862
QY 819 TGATATAAAGAGATACAAAGATTTCAATAGGAAGAATAGTGGCATTAAGAACTGAACCTTAC 878
Db 863 TTTTATATGATAAATAAATTTTGTAAATTA-----TTTAAATTTTATATTTTAAATTTTGTG 917
QY 879 AAGAGAAATTTATACAACACTGAAATAAAATTTTACCGCTCTTACTTACCTTGAAATTCACAC 938
Db 918 TTGTTTTTGTAAATAAATTTTAAAAATAAATTTTATTTTATTTTATTTTAAATGAATAA 977
QY 939 CAATCTCGCTATTAATGGGAATATAATTTTAAACAGGTTACGGCTTAGAATTTTCAATTTT 998
Db 978 AATATATATTAATTTTAAAAATAAATTTTAAAAATAAATTTTAAAAATAAATTTTAAAA 1037
QY 999 AGATGAACTTATATTTTATACAAAAATGAACGTCGCGGAATCGTTTAGTTGGTATTGCG 1058
Db 1038 TTTTGAATTTTAATTAATGTAATAAATAA-----AAAAATTTTGTAAATTTTGTTTTTTTA 1094
QY 1059 GAATCGTAATAGATCTACTTATGCTACGACAGGAATGAAATTTATATATGGAAGAAGAAC 1118
Db 1095 ATGTTTTTAAATGTTATATATTTGTTTTTAAATTTTGTATTTTGAATTTTGAATAAAT 1154
QY 1119 AGGTCACCCCAACAAACAACTTTAATACCAATTTGAAATCCTATAAAGTTTCAATTTGTAAC 1178
Db 1155 ATTAATATATTTTGTGATTTATTAATTTTAAAAATTTTAAATTTTAAATTTTAAATTTAAT 1214
QY 1179 TGATAGACAGTAACCTCCTACTCCCTTTCCCTAACATATACCTTTTACAAATTTAAATCAAT 1238
Db 1215 TTTTAAATAATAAATAAATTTTGTGAATAAATAAATAAATAAATAAATAAATAAATAAATA 1274
QY 1239 TGAACCTTTTATTAATAATTTTCACTAGTAATAATAATAATAATAATAATAATAATAATA 1298
Db 1275 TATAAATAATGTAATATTTTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1334
QY 1299 ATCTAATGATAAATAAACAACACTGATTTTCAATTTTCTGTAAAAAAGAACTGTAAACCAAT 1358
Db 1335 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1394
QY 1359 TATTAAATCCAAATTTGTTTACCAAGCTATAATAGTTATAGTCATATTTTATCCAGCTTTC 1418
Db 1395 AATATGATTTTATTTTATTTTATTTTATTTTAAAAAATAAATAAATAAATAAATAAATAA 1454
QY 1419 TTTATTTAATTTTCTCTATAAATAATTTGGATTAGCGCTAAAT--ATATTATATACAGGTGCA 1476
Db 1455 TTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1514
QY 1477 TTAGATGGAACACAGTAGTGTAAATAGAAATAATGCAATATCAGATAAATAAATAAATAA 1536
Db 1515 ATATAAATATGTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1574
QY 1537 ATGATCCCAAGCAATCAAGGTAAACAGCTTCGATCAAACTCTAAGGTAAATGAAGACCT 1596
Db 1575 TTTAATAATTTTAAATTTATTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1634
QY 1597 GGTTCATACAGGAGGAACCTCGTTTTTATTTACAAAGTCAAGGCGGTTTACAGATTTACATGT 1656
Db 1635 G--TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1692
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	Qy	Db	Qy	Db
736	AATATGAGATGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGAT	736	ATATGAGATGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGAT	736
661	ACTCGAATATGGCAAGATTCAATCAGTTTATAGGAGAGATTTAACTTCTGTATTAGAT	661	ACTCGAATATGGCAAGATTCAATCAGTTTATAGGAGAGATTTAACTTCTGTATTAGAT	720
796	ACTATCGCTCAATTTTCTTTTTTATGATATAAAGAGATA	833	ACTATCGCTCAATTTTCTTTTTTATGATATAAAGAGATA	833
721	ATCGTTGTCTCTTTTCCGAATCTACGATGTAGAACATA	758	ATCGTTGTCTCTTTTCCGAATCTACGATGTAGAACATA	758

Search completed: February 15, 2006, 05:12:27
Job time : 1555 secs

Qy 796 ACTATCGCTCAATTTC TTTTATGATATAAAGAGATA 833
| | | | | | | | | | | | | | |
Db 721 ATCGTTGTCTTTTCCGAACTACGATGTTAGAACA TA 758

RESULT 15
US-10-825-751-7
; Sequence 7, Application US/10825751
; Publication No. US20040194165A1
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: Novel Bacillus thuringiensis Isolate Active Against Lepidopteran
; TITLE OF INVENTION: Pesce, and Genes Encoding Novel Lepidopteran-Active Toxins
; FILE REFERENCE: MA-43CDF2D4
; CURRENT APPLICATION NUMBER: US/10825,751
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 09/837,961
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/521,344
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 08/933,891
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: US 08/356,034
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: US 08/210,110
; PRIOR FILING DATE: 1994-03-17
; PRIOR APPLICATION NUMBER: US 07/865,168
; PRIOR FILING DATE: 1992-04-09
; PRIOR APPLICATION NUMBER: US 07/451,261
; PRIOR FILING DATE: 1989-12-14
; PRIOR APPLICATION NUMBER: US 371,955
; PRIOR FILING DATE: 1989-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 3522
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-825-751-7

Query Match	3.8%;	Score 79.6;	DB 8;	Length 3522;
Best Local Similarity	53.3%;	Pred. No. 0.00024;		
Matches 212;	Conservative 0;	Mismatches 159;	Indels 27;	Gaps 1;
Qy	436	ATACGATTTTCAGAAATGTTTCACATGATTTTATTCGAGAAATACCTGGTTCCCACTTGAA	495	
Db	388	ATTTCGATTTTCCTAATACAGACGACGCTTTTAATAACAGCAATAAATAATTTTACACTTACA	447	
Qy	496	ACTTATAAAAACGCTATTACTACCTATTATTGCGCAAGCTGTAATTTTCATTTTAAATTTA	555	
Db	448	AGTTTTCGAAATCCCTCTTTTATCGGTCATGTTTCAAGGGCGAATTTACATTTATCACTA	507	
Qy	556	TTACAAACAAGTGCTGAATTTGGCTGATGAAATGGAATGCAGATATACATCTCTTCAAAATT	615	
Db	508	TTAAGACACGCTGTATCGTTTGGCGAGGGTTGGGCACTGGGATAVAGCTACTGTGTTAATAAT	567	
Qy	616	GAACCTAATGCTGGAAACATCAGATGACTATATATAAACTTTTAAAGAAATATACCTTAAA	675	
Db	568	C-----AATTATAATAGATTATAAATCTTTATTTCATAGATA	600	
Qy	676	TATAGTAACTATTGTGCAATATACCTATAGAGAAGGACTATAATAAACTTCGAAACGAAACCT	735	
Db	601	TATACGAAAACATTTGTTTGGACACATACAATCNAGGATTAGAAAACCTTAAGAGGTTACTAAT	660	
Qy	736	AATATGATGAGGAGTATATTTAATGATTTATCGAAGATATATGACTATTACTGTATTATAGAT	795	
Db	661	ACTCGACAAATGGGCAAGATTCAATCAGTTTGTAGGAGAGATTTAAACATTTACTGTATTAGAT	720	

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	75.6	3.6	1959	11	US-11-192-801-1	Sequence 1, Appli
2	72.4	3.5	1959	11	US-11-192-801-3	Sequence 3, Appli
C 3	71.8	3.4	171486	11	US-11-121-086-105	Sequence 105, App
C 4 *	71.4	3.4	171486	11	US-11-121-086-25	Sequence 25, Appl
C 5	65.2	3.1	173602	11	US-11-121-086-25	Sequence 25, Appl
C 6	65	3.1	139054	11	US-11-098-686-8738	Sequence 8738, Ap
7	63.8	3.1	171486	11	US-11-121-086-96	Sequence 96, Appl
8	61.8	3.0	173602	11	US-11-121-086-25	Sequence 25, Appl
9	60.8	2.9	139054	11	US-11-121-086-96	Sequence 96, Appl
10	59.4	2.8	158692	11	US-11-121-086-30	Sequence 30, Appl
11	58.6	2.8	2031	11	US-11-058-727-51	Sequence 51, Appl
12	58.6	2.8	2031	11	US-11-058-727-83	Sequence 83, Appl
13	58.6	2.8	2031	11	US-11-108-389-51	Sequence 51, Appl
14	58.6	2.8	2031	11	US-11-108-389-83	Sequence 83, Appl
15	58.6	2.8	2031	11	US-11-224-624-51	Sequence 51, Appl
16	58.6	2.8	2031	11	US-11-224-624-83	Sequence 83, Appl
17	57.4	2.8	2028	11	US-11-058-727-39	Sequence 39, Appl
18	57.4	2.8	2028	11	US-11-058-727-71	Sequence 71, Appl
19	57.4	2.8	2028	11	US-11-108-389-39	Sequence 39, Appl
20	57.4	2.8	2028	11	US-11-108-389-71	Sequence 71, Appl
21	57.4	2.8	2028	11	US-11-224-624-39	Sequence 39, Appl


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Qy 1434 CTATATAAATTGGATTAGCGCTAAATATATATATATATACAGGTGCATTAGGATGGACACAG 1493
Db 17033 CATATATAAATATACAAATATATATCTCATCATATATAAATATACAAATATATTTATATAT 16974
Qy 1494 TAGTGTGTAATAGAAATTAATGCAATATCAGATATAAATAAATTAATGATCCAGCAATCAA 1553
Db 16973 ATCTATCATATATAAATATACAAATATATTTATATATATCTATCATATATAAATATACAA 16914
Qy 1554 AGGTAAACAGCTTGGATACAACTCTAAGGTAATGGAAGGACCTGGTCATACAGAGGAAA 1613
Db 16913 ATATATTTATATATCTATCATATATAAATATATAAATGATTTATATATAAATAATATAA 16854
Qy 1614 CTTGGTTTATTAACAAGTCAAGGGCGTTTAGAGATTTACATGTAGAACTCCTAATTCCTAC 1673
Db 16853 TATATATATATATATAGATAATATATGATATCTATATAATTAATATATAAATATATATAT 16794
Qy 1674 ACAATCTTATTAACATTAAGACTTCGATACGCTACAAATGGTGTGGAATAATCTCTTCCTAA 1733
Db 16793 AATATGTAATGTTATATATGTTATATATTTAAGACATATATAATATATATTAATTAATAA 16734
Qy 1734 TATATCTCT--TACAATAACAGGAGTAATAGGAATACCACTCAACGACTCAACACACT 1791
Db 16733 TATATTTATATATAAATATATATATTAATATATATTTATATATAAATTAATATATTTATTA 16674
Qy 1792 TTTTCTGGTCAAAATTAATAATTTACAATACGAGATTTTGGGTATTTCCAAATTTCCA 1851
Db 16673 TATTAATATGTAATATATATATATATATATAAATAATATATATAATATATATATATATAT 16614
Qy 1852 AGTACAGTAACATTACCTTTAAATCGAAACATACCATTTATTTAATTCGTGCA-GAATG 1910
Db 16613 TATATAATATATATAATATTTATATAAATAATATAAATATATAATATATATATATATATAT 16554
Qy 1911 ATCAAAATTCAAATTTAATCATTTGATGATAAATAATTTGAATTTATACCAATTAATCTCTCTGACG 1970
Db 16553 ATTATGATTATATATATATATTTGTTTAAATATATATAAATAATATAATATATAATATATAT 16494
Qy 2027 CCAAAATAGAGA---AAACAAAAATTAGAACTATCCAAACAAATAAATAATACATTTT 207
Db 16493 ATATAAATTTATATATAATATAAATCTTATATAAATTTATATAAATTTATATAAATAATTA 16434
Qy 208 CAAAAATACAAAAAATCTTTAAATATATAAGAGCCACAACTATGATATTTGAT 2082
Db 16433 TAAATATATATATATATAAATTTTAAATATCAATTAATTTATATATATATATATAT 16379
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RESULT 4

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US-11-121-086-25/c
; Sequence 25, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 173602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-25
```

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Query Match 3.4%; Score 71.4; DB 11; Length 173602;
Best Local Similarity 42.5%; Pred. No. 0.00011;
Matches 551; Conservative 0; Mismatches 736; Indels 8; Gaps 3;
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Qy 737 ATATGAGATGGAGTATTTAATGATTTATCGAAGATATATGACTATTAATCTGTTATGAGATA 796
Db 137315 ATATAATATATATATATATAAATTTATATATATATATATATATATATATATATATAT 137256
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Qy 797 CTATCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGATAG 856
Db 137255 ATATATATATATTTATATATACATATTTATATATATATATATATATATATATATATAT 137196
Qy 857 GTGGCAATTAACACTGAACTTACAAGAGAAATTTTATACAACTGAAATAAATTTTGACCGTC 916
Db 137195 ATATAATATATGATATATAATTTATATAATATATACATATATAATATATGTTGATATAAT 137136
Qy 917 TTACTTTACCTTGAATTTCAACCCAACTCGCTATAATGGAATATAATTTTAAACACGTTTCA 976
Db 137135 ATAAATATATACATATATATAATATGTTGATATAATATATATATATATATATATATATAT 137076
Qy 977 GGCTTAGATATATTTTCATTTTGTAGATGAATTTATTTTATACAAAAAATGAAACGPAAG 1036
Db 137075 GTATATAATTTATATAATTTATATACATATATTTATATATTTATATTAATTAATATA 137016
Qy 1037 GGAATCGTTTGTGTTGTAATTCGGAATCGTAATGAGACTTATGCTACGACAGGAAGTCTG 1096
Db 137015 ATATAAATATATATATATATATATATATATATATATATATATATATATATATATATA 136956
Qy 1097 AATTTATATATGAGAAAGAACAGGTCACCCACAAACAAACAACTTTTAAATACCATTTGAA 1156
Db 136955 TAATAATATATAAATATATTTATATATAATATAATATAAACAATATATATATATA 136896
Qy 1157 CCTATAAAGTTTCAA--TTGTAACTGTAGACAAAGTAACTCCTACTTCCCTTTTCCCTAAC 1215
Db 136895 TATATAATATATAAACAATATTTATATAAATATATATATATATATATAAACAATATATA 136836
Qy 1216 ATATACCTTTACAATTAATCAAAATTTGAACCTTTTATTTAAATTAATTTCCACTAGTAATA 1275
Db 136835 ATATAAATATATAAACAATATTTATATAAATAATATAAATATATAAACAATATATAAAT 136776
Qy 1276 ACATATTCAGCTGGGGGAATTTTCTAATGATATAAATAAACAACACTGATTTTCAATTTCC 1335
Db 136775 ATATAAATATATAAACAATATTTATATAAATATAATATAAATATATAAATATATA 136716
Qy 1336 GTAAAAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCAAGCTAATAATAGTTAT 1395
Db 136715 TAATATATAAATAATATATTTATATAAATATAAATATAAATATAAATATAAATAATA 136656
Qy 1396 AGTCATATTTTATCCAGTTTTCTTTATTTTAAATTTATTTCCCTATAAATAATTTGGATTAG 1455
Db 136655 TATATATATAAATAATATAAACAATATTTATATAAATAATTTATATAAATAATATAA 136596
Qy 1456 AATATATATATACAGGTGCATTAGGATGGACACACAGTAGTGTGTTAATAGAAATAATGCA 1515
Db 136595 AATATATTTTATATATATATTTTATATACATAAACAATATAAATAATATAAATAATATA 136536
Qy 1516 ATATCAGATAAATAAATTAACAAATGATCCAGCAATCAAAAGGTAAACAGTCTTTGTATACA 1575
Db 136535 ATATAAATAATATATATAAATAATATAAATAATATAAATAATATAAATAATATAAATA 136476
Qy 1576 TCTAAGGTAAATGAAGGACCTGGTCATACAGAGGAAACCTTTGGTTTATTTTACAAAGTCAA 1635
Db 136475 TTATATAGATTTTATATAAATTTTATATAATTTTATATAATTTTATATAATTTTATATA 136416
Qy 1636 GGGGTTTAGAGATTACATGTAGAACTCCTAATTTCTACACAACTCTTATTTACATAGACTT 1695
Db 136415 TATATATATATAAATTTTATATAATTTTATATAATTTTATATAATTTTATATAATTTTAT 136356
Qy 1696 CGATACGCTACAAA-----TGGTGTGGAATAATCTCTTCCCTAATATATATCTCTTACAATA 1749
Db 136355 ATATATATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAATATAAATA 136296
Qy 1750 CCAGAGTAATAGGAATACCACTCAACGACTCAACAAACACTTTTCTGGTACAAATATAT 1809
Db 136295 TTATATATATATAAATAATATAAATTTTATATAAATTTTATATAATTTTATATAAATAAT 136236
Qy 1810 AATAATTTACATACGGAGATTTTGGGTATTTCCAAATTTCCAAAGTACAGTAACTTACCT 1869
Db 136235 ATAATTTATATATATTTTATATAAATAATATAAATTTTATATAATTTTATATAAATAAT 136176
```


QY	598	ATACATCCCTTGC	AAATTTGAACCTTAATCTCGGAACATCAGATGACTATTATTAACCTTTTA	657
DB	43923	ATAAATTTAAATATAAAATATAAAATTTAAAT	-----ATATATTTAAATATATATGTTTAAATATTTTTAA	43868
QY	658	AAAGAAATATATACCTTAAATATATAGTAACTATTGTGCAATACCTATAGAGAAGGACTAAAT		717
DB	43867	TATAAATGCATATATATATATATGTAATATATTTTAAAGTATAAATATGACATATTTGTATAT		43808
QY	718	AAACTTCGAAACGAACTTAATATAGATGGAGTATATTTTAATGATATATCGAAGATATATG		777
DB	43807	TAAATACATATCTGTATATATATATATATATATATTTAAATTTAAATATAATATATCTATATATTT		43748
QY	778	ACTATTACTGTAATAGATACCTATCCGTCCAATTTCTTTTATGATATAAAGAGATACAAA		837
DB	43747	TATATAAATTTATATATCTTATAAATATATATATATATATACATAAATATATGACATGTAAT		43688
QY	838	GATTCAAATAGGAAGAATAGGTGGC-ATTAAAACTGAACCTTCAAGAGAGAAATTTATACAAC		896
DB	43687	TATATATTTATATATAAATTAATATATATATATATATTTATATATATTTCTATTAA		43628
QY	897	TGAAATAAATTTTGGCCGCTTTACTTACCTTGAAATTCACCCCAATCCGCTATAATGGGA		956
DB	43627	TATTATTAATATTAATTAATTAATTAATATATATATATTAATTAATTAATATATTTA		43568
QY	957	ATATAAATTTAAACAGCTTCAGGCTTAGATATTTTCATTTTTTAGATGAACCTTATTTTA		1016
DB	43567	TTATATTTTAAATATAAATCTATATCTTCATTTTTTATAAATTTTAAATTTATGTTATTA		43508
QY	1017	TACA---AAATGAAACGTACGGGAATCGTTTACTGTTGTTGGAATCGTAATAGATC		1073
DB	43507	AATATATAAATTTATATGTTGATTAATTTATATAAGTATATGGAATGTAATTTAAAT		43448
QY	1074	TACTTATGCTACGACAGGAACCTGAAATTTATATATGAGAGAAACAGGTCACCCACAAC		1133
DB	43447	ATATATTTTATATATTTTAAATTAACATTTTAAATTTTATAATTTTAAATTTTAAAT		43388
QY	1134	AAAACTTTAATACCAATTTGGAATCCCTATAAGTTTCAATTTGAACTGATAGACAGTAAC		1193
DB	43387	ATGAAATTTTATAAATTTTATAAATTTAAATATAAATTAATATTTATTTATTAATAGT		43328
QY	1194	TCCTACTTCCCTTTTCCCTTAAACATATACCTTTACAAATTAATCAAAATTTGAATTTTAA		1253
DB	43327	AATTAATATATATATATATATATATATATAAATTTATATTTATTAATTAATTAATTAAT		43268
QY	1254	TAATTCACCTAGTAATAAATTAACATATTTCAAGCTGGGGGAATTTTCTTAATGATAAAAA		1313
DB	43267	ATATTATATAAATTTATTAATTAACATATAATATATGTTATATATAAATTAATAAATTA		43208
QY	1314	ARCAACTGATTTTCAATTT		1332
DB	43207	TATAAATTTAGCAAAACATTT		43189

```

RESULT 7
US-11-121-086-105
; Sequence 105, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105
; LENGTH: 171486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-105

```

	Query Match	3.1%; Score 63.8; DB 11; Length 171486;
	Best Local Similarity	42.7%; Pred. No. 0.0031;
	Matches 506; Conservative	0; Mismatches 667; Indels 12; Gaps 3;
QY	283 ATAAACAGCTAAGTTTACAACCTTTAGAAGGATTTAGACAAAATTATTCACAAAGCTATAAT	342
DB		
QY	16332 ATATTAATATATATTTATGTGAT	16391
DB		
QY	343 ACAGCATTTAGATGATTTGGAGAAAAATTAAAAAGACTCACAGCTCCTGGATTACCACCATCA	402
DB		
QY	16392 AFAATATTTTGATATTTATAAAATTATATAAATATATAAATTTATATAATATTTATATAAATATA	16451
DB		
QY	403 TCAGCATTTACAACAAGCTGCCTTGACICTTAAAAATACGATTTTGAGATGTTTCACAAATGAT	462
DB		
QY	16452 ATATAAATTTATATAAAGATTTATATTTATATATATATATATATATATATATATATATATAT	16511
DB		
QY	463 TTTATTTTCGAGAAATACCTGGTTTTCCAACTTCGAACCTTATAAACGCTATTACTACCTATT	522
DB		
QY	16512 TATATTTAATATATTTAAAAACAAT	16571
DB		
QY	523 TATGCGCAAGCTGCTAAATTTTTCATTTTAAATTTTATTTACAAAGGTGCTGAAATTCGGCTGAT	582
DB		
QY	16572 TAT---ATATATATATTTTATATAATTTATATATATATATATATATATATATATATATATAT	16627
DB		
QY	583 GAATGGAATGCGAGATPATACCTCTTCCAATAATGGAACCTAAATGCTGGAGACATCAGATGAC	642
DB		
QY	16628 ATATTATATATATTTTATTATATAGTATATAATATATTTACATATTTAATAATAATAATATATTA	16687
DB		
QY	643 TATTTATAAATCTTTAAAAAGAAAAATATACCTAAATATAGTAACTATGTCGAAATACCTTAT	702
DB		
QY	16688 ATTATATATAAATATATTTAATAATATATATATATAATAATAATATATTAATTAATATATAT	16747
DB		
QY	703 AGAGAAGGACTAAATAAACTTCGAAACGAACTAAATATGAGATGGAGTATATTTTAATGAT	762
DB		
QY	16748 ATATTTATATGCTTTAATAATATATBAACATATAATACATTTACATATATATATATATATATAT	16807
DB		
QY	763 TATCGAAGATATATGACTATTTACTGTATTAGATACTATCGCTCAATTTCTTTCTTTTATGAT	822
DB		
QY	16808 TATATAATTTATAGATAATACATATATTTCTATATAATAATAATAATAATAATAATAATAATAAT	16867
DB		
QY	823 ATAAAGAGATACAAAGATTTCAAATAGGAAGAATAGTGGCAATTTAAACTTGAACCTTACAGA	882
DB		
QY	16868 ATAATAACATTTATATAITTTATATATGATAGATATATAATAATAATAATAATAATAATAATAAT	16927
DB		
QY	883 GAAATTTTACAACTCGMAATAAATTTTCAGCGCTCTTACTTACCTTGGAAATTTCAACCCCAAT	942
DB		
QY	16928 ATGATAGATATATATAAATATATTTTGTATATTTATATATATATATATATATATATATATATAT	16987
DB		
QY	943 CTCGCTATAATGGAATATAAATTTTAAACAGCTTCAGGGCTTAGAT-----TATTTTCATT	996
DB		
QY	16988 TTGTATATTTATATATGATAGATATATATTTTGTATATTTATATATATATATATATATATATATAT	17047
DB		
QY	997 TTAGATGAACTTATATATTTTATATCAAAAAATGAAACGTACGGGAATTCGTTTAGTTCGGTATT	1056
DB		
QY	17048 ATATAITTTTATATATAGATATATATAAAATTTTATATATTTTATATATTTATAGATATATAT	17107
DB		
QY	1057 GCGAATTCGTAANTAGATCTTACTTATGCTACGACAGGAACCTGAAATTTATATATGCGAAGA	1116
DB		
QY	17108 AAAATATATTTATATATTTTATATATATAGATATATAAAATATATTTTATATATTTTATATAT	17167
DB		
QY	1117 ACAGGTCGCCCAACAACAAAACTTTAAAPACCAATTTGAACTCCTATAAAGTTTCAATTTGTA	1176
DB		
QY	17168 ATAGATATATATBAATATATTTTATATATTTTATATATTTATATATATATATATAAATAATTTA	17227
DB		
QY	1177 ACTGATAGACAAGTAACCTCTACTTCCTCCCTTTTCCCTAACATATACCTTTACAATTAATCAA	1236
DB		
QY	17228 TATATTTATATATTTATAGATATATAAATAATAITTTATATATTTTATATATTTATATAGATATA	17287
DB		
QY	1237 ATTTGAACCTTTTATTAATTAATTTCCACTAGTATATAAATTAACATATTCAGCTGGGGGAAT	1296
DB		
QY	17288 TAAATATATTTTATATATTTTATATTTTATGATATATAAATAATAITTTATATATTTTATATA	17347
DB		

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QY 1297 TTATCTAATGATATAAAACAACTGATTTTCATTTTCTGTAAAAAGACTGTAAACCA 1356
DB 17348 TTATAGATATATATAAATATATTTATAGATTTATATATATTATAGATATATA--TAAATATA 17405
QY 1357 ATTATTAATCCAAATTTGTTTACCAAGCTATAATAGTTATAGTCATATTTTATCCCAAGTTT 1416
DB 17406 TTTATAGATTTATATATTATAGATATATATAAATATATTTTATAGATTTATATATTATAGA 17465
QY 1417 TCTTTATTTAAATTTATCTTATATAAAATTTGGATTAGCGCTAAATATA 1461
DB 17466 TATATAAAATATATTTTATAGATTTTATATATATTATAGATATATA 17510

RESULT 8
US-11-121-086-25
; Sequence 25, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 173602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-25

Query Match 3.0%; Score 61.8; DB 11; Length 173602;
Best Local Similarity 44.5%; Pred. No. 0.0075;
Matches 462; Conservative 0; Mismatches 567; Indels 10; Gaps 5;

QY 432 TAAATACGATTTGAGAAATGTTCCAAATGATTTTATTCGAGAAATACCTGGTTTCCAATC 491
DB 136072 TAATATATATATAAATATATATATGTTATATATTTTATATATAAATATATATATATTT 136131
QY 492 TGAACCTTATAAACCTTACTACTCTATTTATGCGCAAGCTGCTAAATTTTCATTAA 551
DB 136132 ATAAATATATAAATATATAATATATATATATATATATATAAATATAAATATATATATA 136191
QY 552 TTATTATCAACAAGGTCGTAATGGCTGATGAATGCAATGCGAGATATACATCCTTCACA 611
DB 136192 TATATAAATATATAATATATATATATATAAATATATAAATATATATATATATATATAA 136251
QY 612 AATTGAACCTTAATGCTGGCAATCAGATGACTTATATAAATTTTAAAAAGAAAAATACC 671
DB 136252 TATATAAATATATAAATATATATATATATATATAAATATATAAATATATAAATATATA 136311
QY 672 TAAATATAGTAATTTGTGCAATACCTATAGAGAGGACTTAATTAACCTCGAAACCA 731
DB 136312 TAAATATATATATAAATATATAATATATATATATATATAAATATATAAATATATAA 136371
QY 732 ACCATAATGAGATGAGTATATTTTAATGATTAATCGAAGATATATGACTATTACTGTATT 791
DB 136372 TTATATATAAATATATAAATATATAAATATATAAATATATAAATATATAAATATATAA 136430
QY 792 AGATACCTGCTCAATTTTCTTTTATGATATATAAAGAGATCAAAAGATTCATAGGAAG 851
DB 136431 ATATAAATATATAAATATATAAATATATAAATCTATATAAATATATAAATATATAAAT 136490
QY 852 AATAGTGGCAT--TAAACCTGAACTTCAAGAGAAATTTTACAACTGGAATAAATTT 908
DB 136491 TAAATAGTATATATATTTATATATATATTTATATAAATATATATATATAGTATATATA 136550
QY 909 TGACCCCTCTTACTTACCTTGAATTCACCCCAATCTCGCTATAATCGGAATATAAATTTAAC 968
DB 136551 TTTATATGTTTATGATATAAATATATAAATATATAAATATATATATATATATATATATT 136610
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QY 969 ACGTTCAGGGCTAGATTTATTTTCATTTTATAGTGAACCTTATATTTTATACAAAAAATGA 1028
DB 136611 TATATAAATATTTTATATAAATATGTTATATATTTTATATAAATATATATATATATATA 136670
QY 1029 AACGTACGGGAATCGTTTGGTTGGTATTCGGAATCGTAATAGATCTTACTTATGCTACGAC 1088
DB 136671 TCGTATATATATAGTATATATATATAAATATATTTTATATATATATATATATATATAT 136730
QY 1089 AGGAACCTGAAATTTATATATGGAGAAAGAACACAGGTCACCCACCAACAAAACTTTAATACC 1148
DB 136731 A-ATATTTATATATATATTTTATAAATATGTTTATATATATATATATATATATAA-T 136788
QY 1149 ATTGGAATCCATAAAGTTTCAATTTGTAACCTGATAGACAAAGTAACTCCCTACTCCCTTT 1208
DB 136789 GTTTATATATTTATATATTTATATAAATATGTTTATATATATATATATATATATATGT 136848
QY 1209 TCCTAACATATATCTTTACAAATTAATCAAAATGAACTTTTATTTTAAATAAATTCACCTAGTAA 1268
DB 136849 TTATAATATATATAATATATTTTATATAATGTTTATATATATATATATATATATATTTA 136908
QY 1269 TAAATTAACATATTCAGCTGGGGGGAATTTTCTAATGATAAAAAACAACCTGATTTTCA 1328
DB 136909 TATAATATGTTTATATATATATATAAATATATATATATATATATATATATATATTTATA 136968
QY 1329 ATTTCTGTAAAAAAGACTGTAAACCAATTTAATCCAAATGTTTGTACCAGCTATAA 1388
DB 136969 ATAT----ATAATATATAAATATAAATATAAATATATATATATATATATATATATATAT 137024
QY 1389 TAGTTATAGTCATATTTTATCCAGTTTTCTTTTATTTTAAATTTTCTATAAATAATTCGATT 1448
DB 137025 TAGTTATATAAATATAAATATAATATATGTTATATAATTTATATAATATATACATATATAT 137084
QY 1449 ACGCGTAAATATATATAT 1467
DB 137085 ATGTATATAAATATATAAT 137103

RESULT 9
US-11-121-086-96
; Sequence 96, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 96
; LENGTH: 139054
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-96

Query Match 2.9%; Score 60.8; DB 11; Length 139054;
Best Local Similarity 45.7%; Pred. No. 0.011;
Matches 406; Conservative 0; Mismatches 467; Indels 15; Gaps 5;

QY 584 AATGGAATGCGATATACATCCCTTCACAAATTTGAACCTTAATGCTGGAACATCGATGACT 643
DB 43306 AATATAAATAAATAATATATTTACTATTATAATAAATAAATAATATATATATATATATATA 43365
QY 644 ATTATAAATTTTAAAGAAATATACCTTAATATAGTAACCTATTGTGCAAAATACCTATA 703
DB 43366 ATTATAAATATAAATTTTCATAATTTTAAATTTAAATTTAAATTTAAATTTAAATGTA 43425
QY 704 GAGAAGGACTAAATAAATCTTCGAAACGAACTTAATATGAGATGGAGTATATTTAATGATT 763
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; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2031)
; US-11-058-727-51

Query Match      2.8%; Score 58.6; DB 11; Length 2031;
Best Local Similarity 46.9%; Pred. No. 0.017;
Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;

QY 214 GACAAACAGTATGGACACAATTTTATAAATGGGAGAAATTTTGTGTATACACCGTTA 273
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
322 GAAAGAGTCAATGGGAAATTTTATGGACAAAGTAGAAGAACTCATTATCAAAAAATA 381
QY ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
274 ACAGAAAGCATAAACAGCTAAAGTTACAACTTTAGAGAGTTTACAGCAAAATATTACAA 333
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
382 GCAGAAATATGCAAGAAATTAAGCGCTTCGGAATTAAGAGGATTAGTAAATATTACCAA 441
QY 334 AGCTATAATACAGCATTAGATGATTGGAGAAATTTAAAGAACTACAAGCTCTCGGATTA 393
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
442 TTATATCTAATCGCTTGAAGATGGAGAAATCCATTTTCGAAGTCGAGGTAGTTTA 501
QY 394 CCACCATCATCAGATTACAAAGCTGCCTTGACTCTTTAAATACGATTTGAGATGTT 453
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
502 AATGGTTCGCGGCAGCCTTACGAGATG-----TGCAGAAATCGATTTGAAATCCTG 552
QY 454 CACAATGATTTTATTCGAGAAATACCTGGTTTCCAATTTGAAACTTTATAAAGCGTATTA 513
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
553 GATAGTTTATTCGCAATATATGCCATCTTTTAGAGTCACAAATTTTGAAGTACCATT 612
QY 514 CTACCTATTATTCGCAAGCTGCTAATTTTCAATTTAAATTTATTATTAACAAGTGTGAA 573
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
613 CTTACTGTATATGCAATGGCAGCAACCTTCACTTTACTGTATTAAAGGACGCGTCAATT 672
QY 574 TTGGCTGATGAATGGAAATGCAGATATACATCTCTTCAAAATTTGAACCTAATGCTGGAACA 633
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
673 TTTGGAGAAATGGGGATGGTCAACAACCT-----ACT 705
QY 634 TCAGATGACTATTATAAATCTTTTAAAGAAATATACCTAAATATAGTAATCTTGCA 693
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
706 ATTAATAACTATTATGATCGTCAAAATGAAACTTTACTGCAGAAATATCTGTATCTGTGA 765
QY 694 AATACCTATAGAGAAGGACTTAAATAAATCTCGAAACGAACTAATATGAGATCGAGTATA 753
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
766 AGTGGTATGAACTGTTTAGCAAAATTAAGAGGACGAGCGCTAAACAATGGGTGAC 825
QY 754 TTTAATGATTATCGAAGATATATGACTATTAATCTGTATTAGATACTATCGCTCAATTTCT 813
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
826 TATAACCAATTCGTGAGAAATGACACTGGCGGTTTTAGATGTTGTGCTATTATTTCCCA 885
QY 814 TTTTATGATATAAGATATAC 834
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

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DB 886 AATTATGACACACGACGTAC 906

RESULT 12
US-11-058-727-83
; Sequence 83, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2031)
; US-11-058-727-83

Query Match      2.8%; Score 58.6; DB 11; Length 2031;
Best Local Similarity 46.9%; Pred. No. 0.017;
Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;

QY 214 GACAAACAGTATGGACACAATTTTATAAATGGGAGAAATTTTGTGTATACACCGTTA 273
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
322 GAAAGAGTCAATGGGAAATTTTATGGAAACAGTAGAAGAACTCATTATCAAAAAATA 381
QY 274 ACAGAAAGCATAAACAGCTAAAGTTACAACTTTAGAGAGTTTACAGCAAAATATTACAA 333
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
382 GCAGAAATATGCAAGAAATTAAGCGCTTCGGAATTAAGAGGATTAGTAAATATTACCAA 441
QY 334 AGCTATAATACAGCATTAGATGATTGGAGAAATTTAAAGAACTACAAGCTCTCGGATTA 393
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
442 TTATATCTAATCGCTTGAAGATGGAGAAATCCATTTTCGAAGTCGAGGTAGTTTA 501
QY 394 CCACCATCATCAGATTACAAAGCTGCCTTGACTCTTTAAATACGATTTGAGATGTT 453
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
502 AATGGTTCGCGGCAGCCTTACGAGATG-----TGCAGAAATCGATTTGAAATCCTG 552
QY 454 CACAATGATTTTATTCGAGAAATACCTGGTTTCCAATTTGAAACTTTATAAAGCGTATTA 513
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
553 GATAGTTTATTCGCAATATATGCCATCTTTTAGAGTCACAAATTTTGAAGTACCATT 612
QY 514 CTACCTATTATTCGCAAGCTGCTAATTTTCAATTTAAATTTATTATTAACAAGTGTGAA 573
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
613 CTTACTGTATATGCAATGGCAGCAACCTTCACTTTACTGTATTAAAGGACGCGTCAATT 672
QY 574 TTGGCTGATGAATGGAAATGCAGATATACATCTCTTCAAAATTTGAACCTAATGCTGGAACA 633
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
673 TTTGGAGAAATGGGGATGGTCAACAACCT-----ACT 705
QY 634 TCAGATGACTATTATAAATCTTTTAAAGAAATATACCTAAATATAGTAATCTTGCA 693
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 706 ATTAATAACTATTATGATCGTCAAAATGAACTTTACTGCGAGATATTTCTGATCACTGTGTA 765
Qy 694 AATACCTATAGAGAAGGACTAAATAAATCTCGAAACGAACCTTAATATGAGATGAGTATATA 753
Db 766 AAGTGTATGAAACTGCTTTAGCAAAATTTAAAGAGGACGAGCGCTTAAACAAATGGGTTGAC 825
Qy 754 TTTAAATGATTATCGAAGATATATGACTATTACTGTATTAGATCTACTCGCTCAATTTTCT 813
Db 826 TATAACCAATTCGTAGAGAAATGACACTGGCGGTTTATAGATGTTGTTGCAATTATTTCCCA 885
Qy 814 TTTTATGATATAAGAGATAC 834
Db 886 AATTATGACACGCGACGTAC 906
RESULT 13
US-11-108-389-51
; Sequence 51, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2031)
US-11-108-389-51
Query Match 2.8%; Score 58.6; DB 11; Length 2031;
Best Local Similarity 46.9%; Pred. No. 0.017;
Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;
Qy 214 GACAAAACAGTATGAGACAAATTTATTAATGGGAGAAATTTTGTGTATACACCGTTA 273
Db 322 GAAAAGAGTCAATGGGAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAAATA 381
Qy 274 ACAGAAAGCATAAACAGCTAAAGTTTAAAGGATTTAGAGGATTTAGACAAATATTACAA 333
Db 382 GCAGAAATGCAAGAAATAAGCGCTTTCCGAATTTAGAGGATTTAGGTAATTAATACCAA 441
Qy 334 AGCTATAATACAGCAATTAGATGATTGGAGAGAAATTTAAAGAGACTTACAGCTCCCTGGATTA 393
Db 442 TTATATCTAATCGCTTGAAGATGGGAAGAAATCCATTTCCGAAGTCGAGGTAGTTTA 501
Qy 394 CCACATCATCAGCAATTACAAAGCTCCCTTGACTCTTAAATAACGATTTGAGAGATGTT 453
Db 502 AATGTTTCCCGCGCAGCTTACGAGATG-----TGCAGAAATCGATTTGAAATCTCG 552
Qy 454 CACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTTGAACTTGAATCTTATAAACCGTATTA 513

Db 553 GATAGTTTATTACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTC 612
Qy 514 CTACCTATTATTATGCGCAAGCTGTAATTTTCAATTTTAAATTTTATTAACAACAAGTGTCTGAA 573
Db 613 CTTACTGTATATGCAATGCGAGCAACCTTCATTTACTGTTTATTAAGGACGCGTCAATT 672
Qy 574 TTGGCTGATGAATGGAATGCAATATACATCTTCTTCAAAATTTGAACCTTAATGCTGGAACA 633
Db 673 TTTGGAGAAAGATGGGATGGTCAACAACT-----ACT 705
Qy 634 TCAGATGACTATTATAAATCTTTTAAAGAAATATATACCTAAATATAGTAACTATTGTGCA 693
Db 706 ATTAATAACTATTATGATCGTCAAAATGAACTTATCTGCAGATATTTCTGATCACTGTGTA 765
Qy 694 AATACCTATAGAGAAGGACTTAAATAAATCTCGAAACGAACCTTAATATGAGATGAGTATA 753
Db 766 AAGTGTATGAACTGCTTTTAGCAAAATTTAAAGAGGACGAGCGCTTAAACAAATGGGTTGAC 825
Qy 754 TTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATCTACTATCGCTCAATTTTCT 813
Db 826 TATAACCAATTCGTAGAGAAATGACACTGGCGGTTTATAGATGTTGTTGCAATTATTTCCCA 885
Qy 814 TTTTATGATATAAGAGATAC 834
Db 886 AATTATGACACGCGACGTAC 906
RESULT 14
US-11-108-389-83
; Sequence 83, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2031)
US-11-108-389-83
Query Match 2.8%; Score 58.6; DB 11; Length 2031;
Best Local Similarity 46.9%; Pred. No. 0.017; Indels 36; Gaps 2;
Matches 291; Conservative 0; Mismatches 294;
Qy 214 GACAAAACAGTATGAGACAAATTTATTAATGGGAGAAATTTTGTGTATACACCGTTA 273
Db 322 GAAAAGAGTCAATGGGAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAAATA 381
Qy 274 ACAGAAAGCATAAACAGCTAAAGTTTAAAGGATTTAGAGGATTTAGACAAATATTACAA 333

```
Db 382 GCAGATATGCAAGGAATTAAGCGCTTCGGAAATTAGAGGATTAGTAAATTAACCAA 441
Qy 334 AGCTATAATACAGCATTTAGATGTTGGAGAAAATTAAGAGCTCAAGCTCCTGGATTA 393
Db 442 TTATACTACTCGCTTGAAGAAATGGGAAGAAATCCATTTGGAAGTCGAGGTAGTTTA 501
Qy 394 CCACCATCATCAGCATTACACAGCTGCCTTGACTCTTAATAATACGATTTGAGATGTT 453
Db 502 AATGGTTCCGGCCAGCCTTTACAGATG-----TGCAGAAATCGATTTGAAATCCTG 552
Qy 454 CACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTTGAAACTTTATAAAGCGCTATTA 513
Db 553 GATAGTTTATTCGCAATATATGCCATCTTTTAGAGTGACAATTTTGAAGTACCAATTC 612
Qy 514 CTACCTATTATTGCGCAAGCTGCTAAATTTTCATTTTAAATTTTATTAACAACAGGTGCTGAA 573
Db 613 CTTACTGTATATGCAATGCGCAGCAACCTTCATTTACTGTATTATAAGAGCGGCTCAATT 672
Qy 574 TTGGCTGATGAATGGAATGCGATATACATCTCTTCAAAATTTGAACCTTAATGCTGGAACA 633
Db 673 TTTGGAGAAGAAATGGGATGGTCAACAACCT-----ACT 705
Qy 634 TCAGATGACTATTATAAACTTTTAAAGAAAATATACCTAAATATAGTAACCTATTCTGCA 693
Db 706 ATTAATACTATTATGATCGTCAAAATGAACCTTCTGCAATATTTCTGATCACTGTGTA 765
Qy 694 AATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACTTAATATGAGATGAGATATA 753
Db 766 AAGTGGTATGAACTGGTTTAGCAAAAATTAAGAGCAGCAGCGCTAAACAATGGGTTGAC 825
Qy 754 TTTAATGATTCGAGATATATGACTATTAATGATTTAGTATTAATGATCTATCGTCAATTTTCT 813
Db 826 TATAACCAATTCGGTAGAGAAATGACACTGGCGGTTTATAGTGTGTTGCAATTAATCCCA 885
Qy 814 TTTTATGATATAAGAGATAC 834
Db 886 AATTATGACACGACGCTAC 906
```

RESULT 15

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US-11-224-624-51
; Sequence 51, Application US/11224624
; Publication No. US20060021096A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Andre
; APPLICANT: Dong, Hua
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert
; APPLICANT: McCutchen, Billy P.
; APPLICANT: Rice, Janet
; APPLICANT: Schepers, Eric
; APPLICANT: Wong, James
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/297402
; CURRENT APPLICATION NUMBER: US/11/224,624
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 10/746,914
; PRIOR FILING DATE: 2003-12-24
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
```

```
; LOCATION: (1)....(2031)
US-11-224-624-51
```

```
Query Match 2.8%; Score 58.6; DB 11; Length 2031;
Best Local Similarity 46.9%; Pred. No. 0.017;
Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;
```

```
Qy 214 GACAAAACGATATGACACAAATTTTAAATGGGAGAAATTTTGTTCATACACCGTTA 273
Db 322 GAAAAAGCTCAATGGGAAATTTTATGGAAACAAGTAGAAGAACTCATTAATCAAAAAATA 381
Qy 274 ACAGAAAGCATAAAAACAGCTAAAGTTTACAACTTTTAGAGAGGATTTAGACAAAATATTACAA 333
Db 382 GCAGATATGCAAGAAATTAAGCGCTTTCCGAAATTAGAAGGATTAGTAAATTAATTAACCAA 441
Qy 334 ACCTATAATACAGCATTTAGATGATTTGGAGAAAATTTAAAGAAGCTCAAGCTCCTGGATTA 393
Db 442 TTATATCTAACTGCGCTTGAAGAAATGGGAAGAAATCCATTTTGAAGTCGAGGTAGTTTA 501
Qy 394 CCACCATCATCAGCATTAACAACAGCTGCCTTGACTCTTAAATATAGGATTTGAGATGTT 453
Db 502 AATGGTTCCGGCCAGCCTTACGATG-----TGCAGAAATCGATTTGAAATCCTG 552
Qy 454 CACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTTGAACTTTATAAAGCGCTATTA 513
Db 553 GATAGTTTATTCGCAATATATGCCATCTTTTAGAGTGACAATTTTGAAGTACCAATTC 612
Qy 514 CTACCTATTATTGCGCAAGCTGCTAAATTTTCATTTTAAATTTTATTAACAACAGGTGCTGAA 573
Db 613 CTTACTGTATATGCAATGCGCAGCAACCTTCATTTACTGTATTATAAGAGCAGCGCTCAATT 672
Qy 574 TTGGCTGATGAATGGAATGCGATATACATCTCTTCAAAATTTGAACCTTAATGCTGGAACA 633
Db 673 TTTGGAGAAGAAATGGGATGGTCAACAACCT-----ACT 705
Qy 634 TCAGATGACTATTATAAACTTTTAAAGAAAATATACCTAAATATAGTAACCTATTCTGCA 693
Db 706 ATTAATACTATTATGATCGTCAAAATGAACCTTCTGCAATATTTCTGATCACTGTGTA 765
Qy 694 AATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACTTAATATGAGATGAGATATA 753
Db 766 AAGTGGTATGAACTGGTTTAGCAAAAATTAAGAGCAGCAGCGCTAAACAATGGGTTGAC 825
Qy 754 TTTAATGATTCGAGATATATGACTATTAATGATTTAGTATTAATGATCTATCGTCAATTTTCT 813
Db 826 TATAACCAATTCGGTAGAGAAATGACACTGGCGGTTTATAGTGTGTTGCAATTAATCCCA 885
Qy 814 TTTTATGATATAAGAGATAC 834
Db 886 AATTATGACACGACGCTAC 906
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Search completed: February 15, 2006, 03:05:11

Job time : 434 secs